

FIG. 1

Enzymes : 36 of 538 enzymes (Filtered)

Settings : Circular, Certain Sites Only, Standard Genetic Code

PstI

GAAACCAGCAGCGGCTATCCGCGCATCCATGCCCCGAAGTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAGGC
CTTTGGTCGTCGCCGATAGGCGCGTAGGTACGGGGGCTTGACGTCTCACCCCTCCGTGCTACCGGCGAAACCAGCTCCG 2800

BamHI

GGATCCTAGCAGAAAAATAAGACTTGATTCCCCCTTAAAATTACAACTGCTAGAAAATGAATGGCTCTCCCGCCTTTTTT
CCTAGGATCGTCTTTTTATTCTGAACATAAGGGGAATTTTAATGTTGACGATCTTTTACTTACCGAGAGGGCGGAAAAAA 2880

BLV Promoter

NarI

PvuII

GAGGGGGAATCATTTGTATGAAAGATCATGCCGACCTAGGCGCCGCCACCGCCCCGTAAACCAGACAGAGACGTCAGCTG
CTCCCCCTTAGTAAACATACTTTCTAGTACGGCTGGATCCGCGGCGGTGGCGGGGCATTTGGTCTGTCTCTGCAGTCGAC 2960

BLV Promoter

PvuII

CCAGAAAAGCTGGTGACGGCAGCTGGTGGCTAGAATCCCCGTACCTCCCCAACTTCCCCTTTCCCGAAAAATCCACACCC
GGTCTTTTCGACCACTGCCGTCGACCACCGATCTTAGGGGCATGGAGGGGTGAAGGGGAAAGGGCTTTTATAGGTGTGGG 3040

BLV Promoter

NaeI

TGAGCTGCTGACCTCACCTGCTGATAAATTAATAAAATGCCGGCCCTGTGAGTTAGCGGCACCAGAAGCGTTCTTCTCC
ACTCGACGACTGGAGTGGACGACTATTTAATTATTTTACGGCCGGGACAGCTCAATCGCCGTGGTCTTCGAAGAAGAGG 3120

BLV Promoter

XhoI

HindIII

TGAGACCCTCGTGCTCAGCTCTCGGTCTGCCTCGAGAAGCTTGTATCACAAGTTTGTACAAAAAGCTGAACGAGAAA
ACTCTGGGAGCACGAGTCGAGAGCCAGGACGGAGCTCTTCAACAATAGTGTTCAAACATGTTTTTTCGACTTGCTCTTT 3200

BLV Promoter

Gateway

att R1

FIG. 2

SEQUENCE LISTING -- TAX [Bovine leukemia virus]

LOCUS AAF97920 309 aa
ACCESSION AAF97920

NUCLEOTIDE SEQUENCE (SEQ ID NO:2):

ATG GCA AGT GTT GTT GGT TGG GGG CCC CAC TCT CTA CAT GCC TGC CCG
GCC CTG GTT TTG TCC AAT GAC GTC ACC ATC GAT GCC TGG TGC CCC CTC
TGC GGG CCC CAT GAG CGA CTC CAA TTC GAA AGG ATC GAC ACC ACG CAC
ACC TGC GAG ACC CAC CGT ATC ACC TGG ACC GCC GAT GGA CGA CCT TTC
GGC CTC AAT GGA GCG CTG TTC CCT CGA CTG CAT GTC TCC AGA GAC CCG
GCC CCA AGG GCC CGA CGA CTC TGG ATC AAC TGC CCC CTT CCG GCC GTT
CGC GCT CAG CCC GGC CCG GTT TCA CTT TCC CCC TTC GAG CGG TCC CCC
TTC CAG CCC TAC CAA TGC CAA TTG CCC TCG GCC TCT AGC GAC GGT TGC
CCC GTC ATC GGG CAC GGC CTT CTT CCC TGG AAC AAC TTA GTA ACG CAT
CCT TGT CCT CGG AAA GTC CTT ATA TTA AAT CAA ATG GCC AAT TTT TCC
TTA CTC CCC CCC TTC AAT ACC CTC CTT GTG GAC CCC CTC CGG TTG TCC
GTC TTT GCC CCA GAC ACC AGG GGA GCC ATA CGT TAT CTC TCC ACC CTT
TTG ACG CTA TGC CCA GCT ACT TGT ATT CTA CCC CTC GGC GA GCC CTT
CTC TCC TAA TGT CCC CAT ATG TCG CTT TCC CCG GGA CTC CAA TGA ACC
CCC CCT TTC AGA ATT CGA GCT GCC CCT TAT CCA AAC GCC CGG CCT GTC
TTG GTC TGT CCC CGC GAT CGA CCT ATT CCT AAC CGG CCC CCC TTC CCC
ATG CGA CCG GTT ACA CGT ATG GTC CAG TCC TCA GGC CTT ACA GCG CTT
CCT CCA TGA CCC TAC GCT AAC CTG GTC AGA ATT GGT TGC TAG CAG GAA
ACT AAG ACT TGA TTC ACC CTT AAA ATT ACA ACT GTT AGA AAA TGA ATG
GCT CTC CCG CCT TTT TTG

PROTEIN SEQUENCE (SEQ ID NO:7):

MASVVGWGP HSLHACPALVLSNDVTIDAWCPLCGPHERLQFERIDTTHTCETHRITW
TADGRPFGLNGALFPRLHVS RDPAPRARRLWINCP LPAVRAQPGPVSLSPFERSPF
QPYQCQLPSASSDGCPVIGHG LLLPWNNLVTHPCPRKVLILNQMANFSLLPPFNTLLV
DPLRLSVFAPDTRGAIRYLSTLLTLC PATCILPLGEPFSPNPICRFPRDSNEPPLSEF
ELPLIQTPGLSWSVPAIDLFLTGP PSPCDRLHVWSSPQALQRFLHDPTLTW
SELVASRKLR LDSPLKLQLLENEWLSRLF

FIG. 3

SEQUENCE LISTING -- HTLV-1 Promoter sequence (SEQ ID NO:4)

```
1  TGACAATGAC CATGAGCCCC AAATATCCCC CGGGGGGCTTA GAGCCTCTCA GTGAAAAACA
61  TTTCCGTGAA ACAGAAGTCT GAGAAGGTCA GGGCCCAGAA TAAGGCTCTG ACGTCTCCCC
121 CCGGAGGACA GCTCAGCACC AGCTCAGGCT AGGCCCTGAC GTGTCCCCCT AAAGACAAAT
181 CATAAGCTCA GACCTCCGGG AAGCCACCGG GAACCACCCA TTTCTCCCC ATGTTTGTCA
241 AGCCGTCCTC AGGCGTTGAC GACAACCCCT CACCTCAAAA AACTTTTCAT GGCACGCATA
301 CGGCTCAATA AAATAACAGG AGTCTATAAA AGCGTGGGGA CAGTTCAGGA GGG
```

FIG. 4

**SEQUENCE LISTING -- HTLV1 Tax Nucleic Acid (SEQ ID NO:3) and
Protein sequence (SEQ ID NO:8)**

1	ATG	GCC	CAC	TTC	CCA	GGG	TTT	GGA	CAG	AGT	CTT	CTT	TTC	GGA	TAC	45
1	Met	Ala	His	Phe	Pro	Gly	Phe	Gly	Gln	Ser	Leu	Leu	Phe	Gly	Tyr	15
46	CCA	GTC	TAC	GTG	TTT	GGA	GAC	TGT	GTA	CAA	GGC	GAC	TGG	TGC	CCC	90
16	Pro	Val	Tyr	Val	Phe	Gly	Asp	Cys	Val	Gln	Gly	Asp	Trp	Cys	Pro	30
91	ATC	TCT	GGG	GGA	CTA	TGT	TCG	GCC	CGC	CTA	CAT	CGT	CAC	GCC	CTA	135
31	Ile	Ser	Gly	Gly	Leu	Cys	Ser	Ala	Arg	Leu	His	Arg	His	Ala	Leu	45
136	CTG	GCC	ACC	TGT	CCA	GAG	CAT	CAG	ATC	ACC	TGG	GAC	CCC	ATT	GAT	180
46	Leu	Ala	Thr	Cys	Pro	Glu	His	Gln	Ile	Thr	Trp	Asp	Pro	Ile	Asp	60
181	GGA	CGC	GTT	ATC	GGC	TCA	GCT	CTA	CAG	TTC	CTT	ATC	CCT	CGA	CTC	225
61	Gly	Arg	Val	Ile	Gly	Ser	Ala	Leu	Gln	Phe	Leu	Ile	Pro	Arg	Leu	75
226	CCC	TCC	TTC	CCC	ACC	CAG	AGA	ACC	TCT	AAG	ACC	CTC	AAG	GTC	CTT	270
76	Pro	Ser	Phe	Pro	Thr	Gln	Arg	Thr	Ser	Lys	Thr	Leu	Lys	Val	Leu	90
271	ACC	CCG	CCA	ATC	ACT	CAT	ACA	ACC	CCC	AAC	ATT	CCA	CCC	TCC	TTC	315
91	Thr	Pro	Pro	Ile	Thr	His	Thr	Thr	Pro	Asn	Ile	Pro	Pro	Ser	Phe	105
316	CTC	CAG	GCC	ATG	CGC	AAA	TAC	TCC	CCC	TTC	CGA	AAT	GGA	TAC	ATG	360
106	Leu	Gln	Ala	Met	Arg	Lys	Tyr	Ser	Pro	Phe	Arg	Asn	Gly	Tyr	Met	120
361	GAA	CCC	ACC	CTT	GGG	CAG	CAC	CTC	CCA	ACC	CTG	TCT	TTT	CCA	GAC	405
121	Glu	Pro	Thr	Leu	Gly	Gln	His	Leu	Pro	Thr	Leu	Ser	Phe	Pro	Asp	135
406	CCC	GGA	CTC	CGG	CCC	CAA	AAC	CTG	TAC	ACC	CTC	TGG	GGA	GGC	TCC	450
136	Pro	Gly	Leu	Arg	Pro	Gln	Asn	Leu	Tyr	Thr	Leu	Trp	Gly	Gly	Ser	150
451	GTT	GTC	TGC	ATG	TAC	CTC	TAC	CAG	CTT	TCC	CCC	CCC	ATC	ACC	TGG	495
151	Val	Val	Cys	Met	Tyr	Leu	Tyr	Gln	Leu	Ser	Pro	Pro	Ile	Thr	Trp	165
496	CCC	CTC	CTG	CCC	CAC	GTG	ATT	TTT	TGC	CAC	CCC	GGC	CAG	CTC	GGG	540
166	Pro	Leu	Leu	Pro	His	Val	Ile	Phe	Cys	His	Pro	Gly	Gln	Leu	Gly	180
541	GCC	TTC	CTC	ACC	AAT	GTT	CCG	TAC	AAG	CGA	ATA	GAA	GAA	CTC	CTC	585
181	Ala	Phe	Leu	Thr	Asn	Val	Pro	Tyr	Lys	Arg	Ile	Glu	Glu	Leu	Leu	195
586	TAT	AAA	ATT	TCC	CTT	ACC	ACA	GGG	GCC	CTA	ATA	ATT	CTA	CCC	GAA	630
196	Tyr	Lys	Ile	Ser	Leu	Thr	Thr	Gly	Ala	Leu	Ile	Ile	Leu	Pro	Glu	210
631	GAC	TGT	TTG	CCC	ACC	ACC	CTT	TTC	CAG	CCT	GTT	AGG	GCA	CCC	GTC	675
211	Asp	Cys	Leu	Pro	Thr	Thr	Leu	Phe	Gln	Pro	Val	Arg	Ala	Pro	Val	225
676	ACG	CTA	ACA	GCC	TGG	CAA	AAC	GGC	CTC	CTT	CCG	TTC	CAC	TCA	ACC	720
226	Thr	Leu	Thr	Ala	Trp	Gln	Asn	Gly	Leu	Leu	Pro	Phe	His	Ser	Thr	240
721	CTC	ACC	ACT	CCA	GGC	CTT	ATT	TGG	ACA	TTT	ACC	GAT	GGC	ACG	CCT	765
241	Leu	Thr	Thr	Pro	Gly	Leu	Ile	Trp	Thr	Phe	Thr	Asp	Gly	Thr	Pro	255

FIG. 5

766	ATG	ATT	TCC	GGG	CCC	TGC	CCT	AAA	GAT	GGC	CAG	CCA	TCT	TTA	GTA	810
256	Met	Ile	Ser	Gly	Pro	Cys	Pro	Lys	Asp	Gly	Gln	Pro	Ser	Leu	Val	270
811	CTA	CAG	TCC	TCC	TCC	TTT	ATA	TTT	CAC	AAA	TTT	CAA	ACC	AAG	GCC	855
271	Leu	Gln	Ser	Ser	Ser	Phe	Ile	Phe	His	Lys	Phe	Gln	Thr	Lys	Ala	285
856	TAC	CAC	CCC	TCA	TTT	CTA	CTC	TCA	CAC	GGC	CTC	ATA	CAG	TAC	TCT	900
286	Tyr	His	Pro	Ser	Phe	Leu	Leu	Ser	His	Gly	Leu	Ile	Gln	Tyr	Ser	300
901	TCC	TTT	CAT	AAT	TTA	CAT	CTC	CTG	TTT	GAA	GAA	TAC	ACC	AAC	ATC	945
301	Ser	Phe	His	Asn	Leu	His	Leu	Leu	Phe	Glu	Glu	Tyr	Thr	Asn	Ile	315
946	CCC	ATT	TCT	CTA	CTT	TTT	AAC	GAA	AAA	GAG	GCA	GAT	GAC	AAT	GAC	990
316	Pro	Ile	Ser	Leu	Leu	Phe	Asn	Glu	Lys	Glu	Ala	Asp	Asp	Asn	Asp	330
991	CAT	GAG	CCC	CAA	ATA	TCC	CCC	GGG	GGC	TTA	GAG	CCT	CCC	AGT	GAA	1035
331	His	Glu	Pro	Gln	Ile	Ser	Pro	Gly	Gly	Leu	Glu	Pro	Pro	Ser	Glu	345
1036	AAA	CAT	TTC	CGC	GAA	ACA	GAA	GTC	TGA							1070
346	Lys	His	Phe	Arg	Glu	Thr	Glu	Val	TRM							354

FIG. 5 (Cont.)

SEQUENCE LISTING -- HIV Promoter sequence (SEQ ID NO:5)

1	CTGGAAGGGC	TAATTTGGTC	CCAAAGAAGA	CAAGAGATCC	TTGATCTGTG	GATCTACCAC
61	ACACAAGGCT	ACTTCCCTGA	TTGGCAGAAT	TACACACCAG	GGCCAGGGAT	CAGATATCCA
121	CTGACCTTTG	GATGGTGCTT	CAAGCTAGTA	CCAGTTGAGC	CAGAGAAGGT	AGAAGAGGCC
181	AATGAAGGAG	AGAACAACAG	CTTGTTACAC	CCTATGAGCC	TGCATGGGAT	GGAGGACGCG
241	GAGAAAGAAG	TGTTAGTGTG	GAGGTTTGAC	AGCAAAC TAG	CATTTTCATCA	CATGGCCCGA
301	GAGCTGCATC	CGGAGTACTA	CAAAGACTGC	TGACATCGAG	CTTTCTACAA	GGGACTTTCC
361	GCTGGGGACT	TTCCAGGGAG	GCGTGGCCTG	GGCGGGACTG	GGGAGTGGCG	TCCCTCAGAT
421	GCTGCATATA	AGCAGCTGCT	TTTTGCCTGT	ACTGGG		

FIG. 6

**SEQUENCE LISTING -- HIV Tat nucleic acid (SEQ ID NO:6) and amino
acid (SEQ ID NO:9) of HIV Tat.**

1	ATG GAG CCA GTA GAT CCT AAT CTA GAG CCC TGG AAG CAT CCA GGA	45
1	Met Glu Pro Val Asp Pro Asn Leu Glu Pro Trp Lys His Pro Gly	15
46	AGT CAG CCT AGG ACT GCT TGT AAC AAT TGC TAT TGT AAA AAG TGT	90
16	Ser Gln Pro Arg Thr Ala Cys Asn Asn Cys Tyr Cys Lys Lys Cys	30
91	TGC TTT CAT TGC TAC GCG TGT TTC ACA AGA AAA GGC TTA GGC ATC	135
31	Cys Phe His Cys Tyr Ala Cys Phe Thr Arg Lys Gly Leu Gly Ile	45
136	TCC TAT GGC AGG AAG AAG CGG AGA CAG CGA CGA AGA GCT CCT CAG	180
46	Ser Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala Pro Gln	60
181	GAC AGT CAG ACT CAT CAA GCT TCT CTA TCA AAG CAA CCC GCC TCC	225
61	Asp Ser Gln Thr His Gln Ala Ser Leu Ser Lys Gln Pro Ala Ser	75
226	CAG TCC CGA GGG GAC CCG ACA GGC CCG ACG GAA TCG AAG AAG AAG	270
76	Gln Ser Arg Gly Asp Pro Thr Gly Pro Thr Glu Ser Lys Lys Lys	90
271	GTG GAG AGA GAG ACA GAG ACA GAT CCG TTC GAT TAG	306
91	Val Glu Arg Glu Thr Glu Thr Asp Pro Phe Asp TRM	102

FIG. 7



FIG. 8

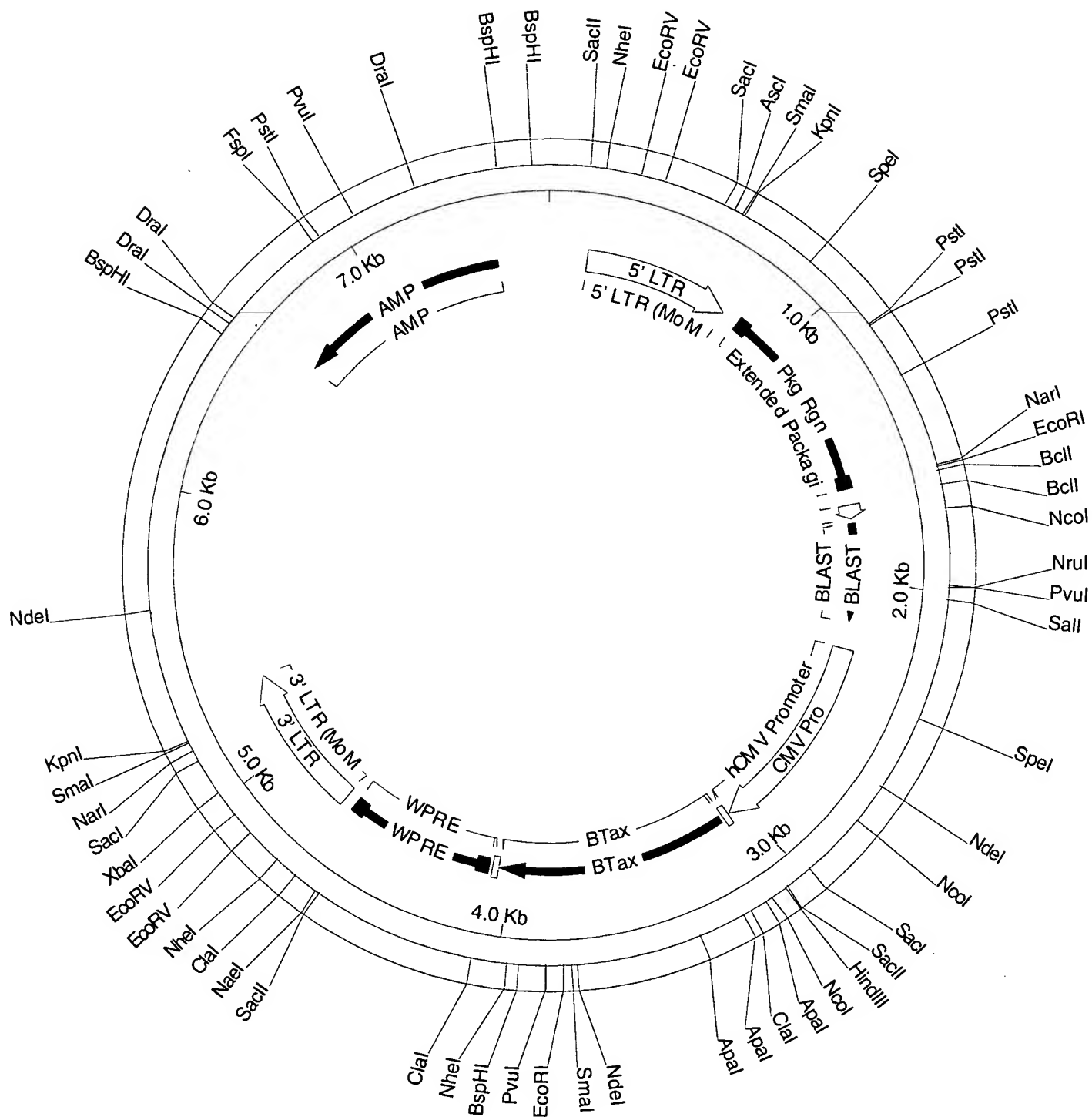


FIG. 9

FIG. 10

Page 1

Friday, November 15, 2002 12:30 PM

pLBC-BTaxW Map.MPD (1 > 7685) Site and Sequence

Enzymes : 35 of 538 enzymes (Filtered)

Settings : Circular, Certain Sites Only, Standard Genetic Code

GAATTAATTCATACCAGATCACCGAAAACGTGCTCTCCAAATGTGTCCCTTCACACTCCCAAATTCGCGGGCTTCTGCCT
CTTAATTAAGTATGGTCTAGTGGCTTTTGACAGGAGGTTTACACAGGGGAGTGTGAGGGTTTAAGCGCCCAAGACGGA

SacII

CTTAGACCACTCTACCCTATTCCCCACACTCACCGGAGCCAAAGCCGCGGCCCTTCCGTTTCTTTGCTTTTGAAGACCC
GAATCTGGTGAGATGGGATAAGGGGTGTGAGTGGCCTCGGTTTCGGCGCCGGAAGGCAAGAAACGAAAACTTTCTGGG

5' LTR

5' LTR (MoMS-

NheI

CACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTC
GTGGGCATCCACCGTTCGATCGAATTCATTGCGGTGAAACGTTCCGTACCTTTTTATGTATTGACTCTTATCTTTTCAAG

5' LTR

5' LTR (MoMSV)

EcoRV

AGATCAAGGTCAGGAACAAAGAAACAGCTGAATACCAACAGGATATCTGTGGTAAGCGGTTCTTGCCCCGGCTCAGGGC
TCTAGTTCCAGTCTTGTCTTTGTGCGACTTATGGTTTGTCTATAGACACCATTCGCCAAGGACGGGGCCGAGTCCCG

5' LTR

5' LTR (MoMSV)

EcoRV

CAAGAACAGATGAGACAGCTGAGTGATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCAAG
GTTCTTGTCTACTCTGTGCGACTCACTACCCGTTTGTCTATAGACACCATTCGTCAAGGACGGGGCCGAGCCCCGGTTC

5' LTR

5' LTR (MoMSV)

AACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATCATCAGATGTTTCCAGGGTGCCCCAAGGACC
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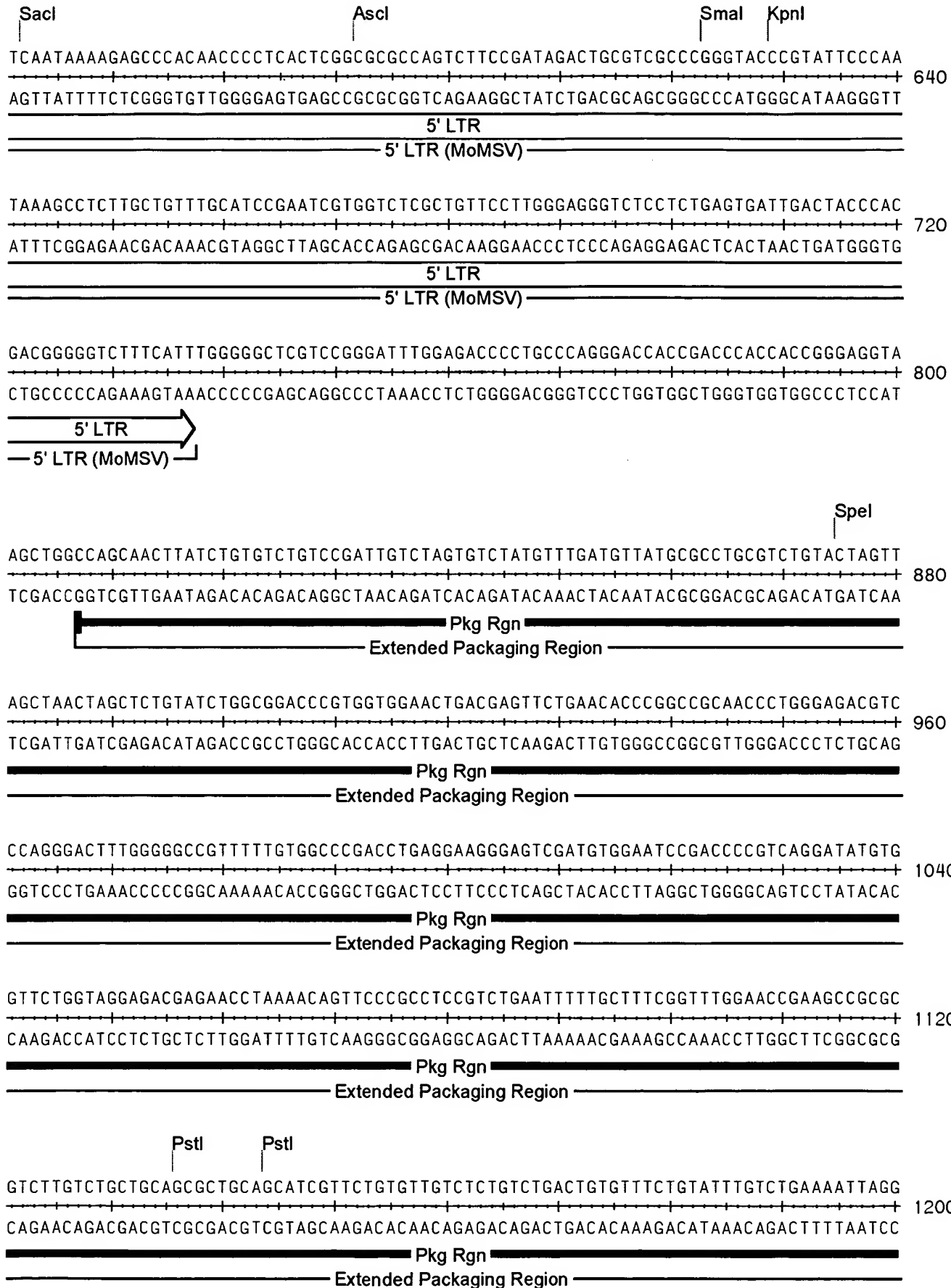
5' LTR

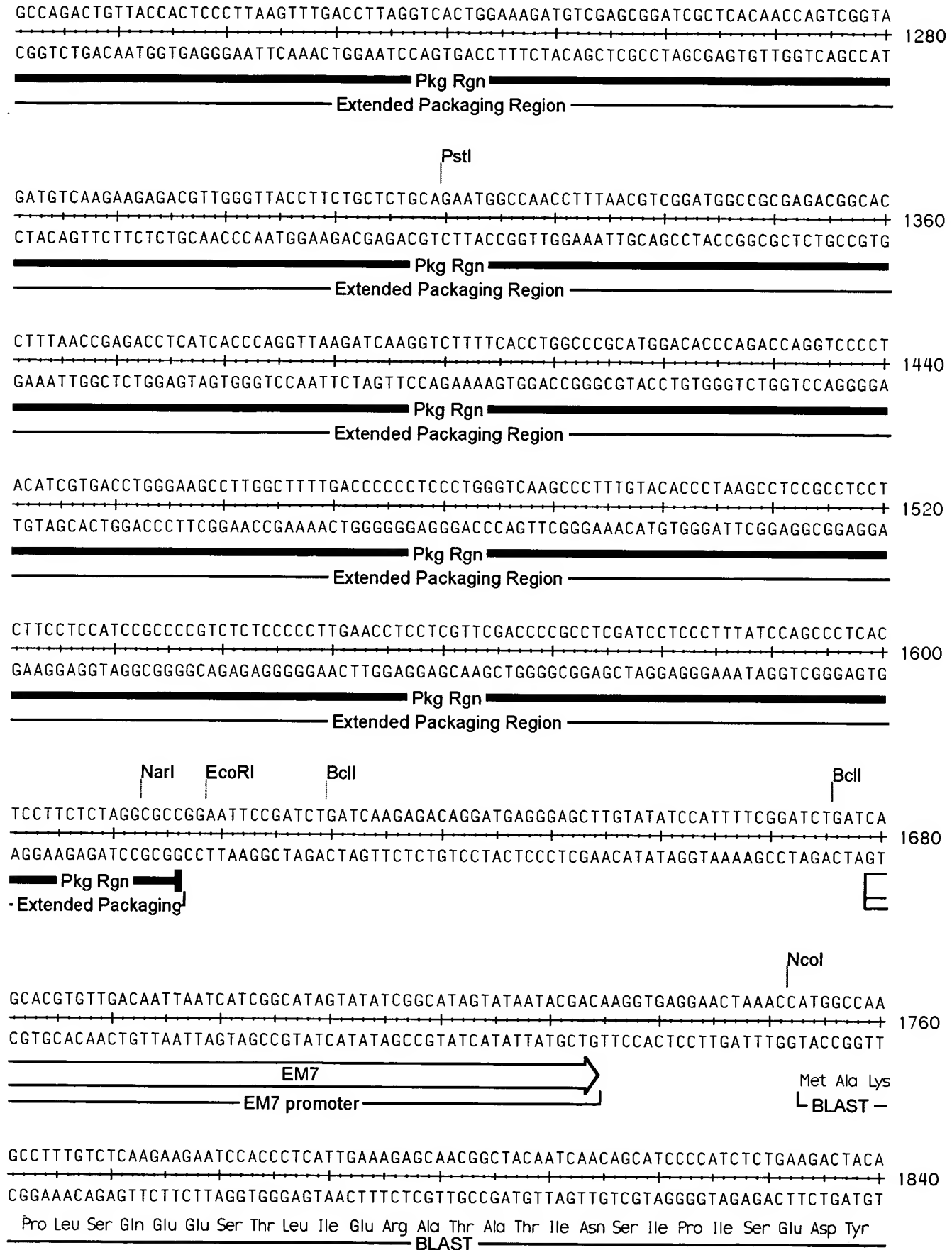
5' LTR (MoMSV)

TGAAAATGACCCTGTACCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCCGCTCTCCGAGC
ACTTTTACTGGGACATGGAATAAACTTGATTGGTTAGTCAAGCGAAGAGCGAAGACAAGCGCGCAAGGCGAGAGGCTCG

5' LTR

5' LTR (MoMSV)





Friday, November 15, 2002 12:30 PM
pLBC-BTaxW Map.MPD (1 > 7685) Site and Sequence

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1920
CGCAGCGGTGCGTTCGAGAGAGATCGCTGCCGGCGTAGAAGTGACCACAGTTACATATAGTAAAATGACCCCTGGAACA
Ser Val Ala Ser Ala Ala Leu Ser Ser Asp Gly Arg Ile Phe Thr Gly Val Asn Val Tyr His Phe Thr Gly Gly Pro Cys
BLAST

GCAGAACTCGTGGTGTCTGGGCACTGCTGCTGCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGCGATCGGAAATGAGAA
2000
CGTCTTGAGCACCACGACCCGTGACGACGACGACGCCGTGACCGTTGGACTGAACATAGCAGCGCTAGCCTTTACTCTT
Ala Glu Leu Val Val Leu Gly Thr Ala Ala Ala Ala Ala Gly Asn Leu Thr Cys Ile Val Ala Ile Gly Asn Glu Asn
BLAST

CAGGGGCATCTTGAGCCCTGCGGACGGTGTGACAGGTGCTTCTCGATCTGCATCCTGGGATCAAAGCGATAGTGAAGG
2080
GTCCCGTAGAACTCGGGACGCTGCCACAGCTGTCCACGAAGAGCTAGACGTAGGACCCTAGTTTCGCTATCACTTCC
Arg Gly Ile Leu Ser Pro Cys Gly Arg Cys Arg Gln Val Leu Leu Asp Leu His Pro Gly Ile Lys Ala Ile Val Lys
BLAST

ACAGTGATGGACAGCCGACGGCAGTTGGGATTCTGTAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTAAGCACTTCGT
2160
TGTCCTACCTGTCGGCTGCCGTCAACCCTAAGCACTTAACGACGGGAGACCAATACACACCCTCCCGATTCTGTGAAGCA
Asp Ser Asp Gly Gln Pro Thr Ala Val Gly Ile Arg Glu Leu Leu Pro Ser Gly Tyr Val Trp Glu Gly
BLAST

GGCCGAGGAGCAGGACTGACACGTGCTACGAGATTTTCGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCG
2240
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2320
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2400
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CMV Pro
hCMV Promoter

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2480
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CMV Pro
hCMV Promoter

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CMV Pro

hCMV Promoter

NdeI

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CMV Pro

hCMV Promoter

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CMV Pro

hCMV Promoter

NcoI

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CMV Pro

hCMV Promoter

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CMV Pro

hCMV Promoter

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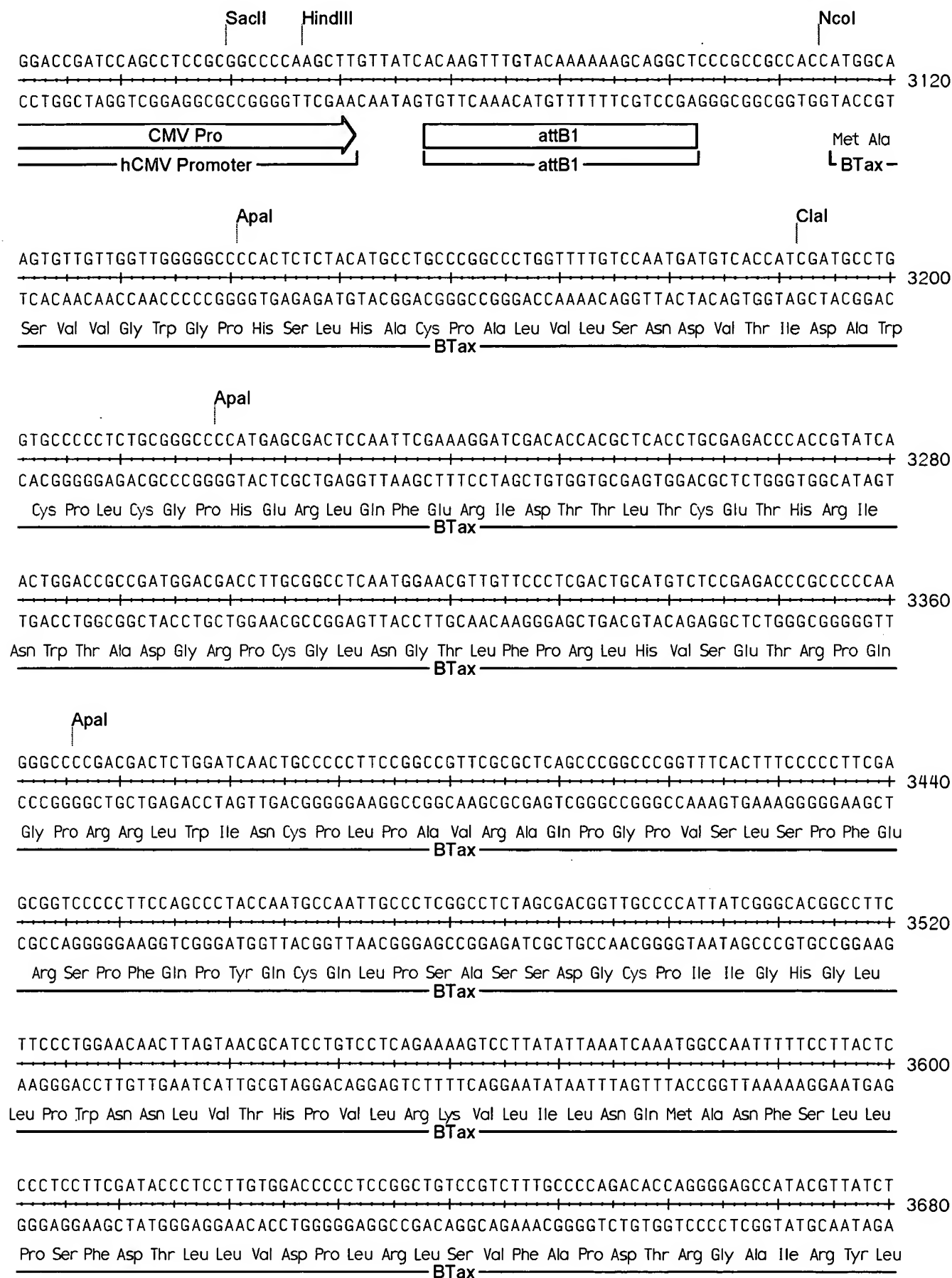
hCMV Promoter

SacI

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CMV Pro

hCMV Promoter



NdeI

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GAGGTGGGAAACTGCGATACGGCCGATGAACATAAGATGGGGATCCGCTCGGGAAGAGAGGATTACAGGGGTATACGG
Ser Thr Leu Leu Thr Leu Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe Ser Pro Asn Val Pro Ile Cys
BTax

SmaI EcoRI

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CGAAAGGGGCCCTGAGGTTACTTGGGGGGAAAGTCTTAAGCTCGACGGGGAATAGGTTTGGGGCCGGACAGAACCAGA
Arg Phe Pro Arg Asp Ser Asn Glu Pro Pro Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser Trp Ser
BTax

PvuI

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CAGGGGCGCTAGCTGGATAAGGATTGGCCAGGGGGAAGGGGTACGTGGCCAATGTGCATACCAGGTCAGGAGTCCGGAA
Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu
BTax

BspHI NheI

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TGTCGCGAAGGAAGTACTGGGATGCGATTGGACCAGGCTTAATCAACGATCGTCTTTTATTCTGAACTAAGGGGAATT
Gln Arg Phe Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys Ile Arg Leu Asp Ser Pro Leu
BTax

ClaI

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Lys Leu Gln Leu Leu Glu Asn Glu Trp Leu Ser Arg Leu Phe attB2
BTax

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WPRE

SacII NaeI

TCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACG 4640
AGTTAGGTCGCCTGGAAGGAAGGGCGCCGGACGACGGCCGAGACGCCGGAGAAGGCGCAGAAGCGGAAGCGGGAGTCTGC
WPRE
WPRE

ClaI

AGTCGGATCTCCCTTTGGGCCGCTCCCCGCTGATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGA 4720
TCAGCCTAGAGGGAAACCGCGGAGGGGCGGACTAGCTATTTTATTTCTAAAATAAATCAGAGGTCTTTTCCCCCCT
WPRE
WPRE

NheI

ATGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGAAGGCATGGAAAAATACATAACTGAG 4800
TACTTTCTGGGGTGGACATCAAACCGTTCGATCGAATTCATTGCGGTAAACGTTCCGTACCTTTTATGTATTGACTC
3' LTR
3' LTR (MoMLV)

EcoRV

AATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTT 4880
TTATCTCTTCAAGTCTAGTTCAGTCCCTTGTCTACCTTGTGCACTTATACCCGGTTTGTCTATAGACACCATTTCGTCAA

3' LTR

3' LTR (MoMLV)

EcoRV

CCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGC 4960
GGACGGGGCCGAGTCCCGTTCTTGTCTACCTTGTGCACTTATACCCGGTTTGTCTATAGACACCATTTCGTCAAGGACG

3' LTR

3' LTR (MoMLV)

XbaI

CCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCC 5040
GGGCCGAGTCCCGTTCTTGTCTACCAAGGGTCTACGCCAGGTCGGGAGTCGTCAAAGATCTCTTGGTAGTCTACAAAGG

3' LTR

3' LTR (MoMLV)

AGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCGCGCG 5120
TCCCACGGGGTTCTGGACTTTACTGGGACACGGAATAAACTTGATTGGTTAGTCAAGCGAAGAGCGAAGACAAGCGCGC

3' LTR

3' LTR (MoMLV)

SacI

NarI

SmaI

CTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGG 5200
GAAGACGAGGGGCTCGAGTTATTTCTCGGGTGTGGGGAGTGAGCCCCGCGGTCAGGAGGCTAACTGACTCAGCGGGCC

3' LTR

3' LTR (MoMLV)

KpnI

GTACCCGTGTATCCAATAAACCCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCCTTGGGAGGGTCTCCTCTGAG 5280
CATGGGCACATAGGTTATTTGGGAGAACGTCAACGTAGGCTGAACACCAGAGCGACAAGGAACCCCTCCAGAGGAGACTC

3' LTR

3' LTR (MoMLV)

TGATTGACTACCCGTCAGCGGGGGTCTTTTCATTTTCCATTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCAGGGAC 5360
ACTAACTGATGGGCAGTCGCCCCAGAAAGTAAAAAGGTAACCCCCGAGCAGGCCCTAGCCCTCTGGGGACGGGTCCCTG

3' LTR

3' LTR (MoMLV)

FIG. 10 (cont)

Friday, November 15, 2002 12:30 PM
pLBC-BTaxW Map.MPD (1 > 7685) Site and Sequence

Page 10

CACCGACCCACCACCGGGAGGTAAGCTGGCTGCCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCT
5440
GTGGCTGGGTGGTGGCCCTCCATTGACCGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGGAGACTGTGTACGTCTGA

CCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCG
5520
GGGCCTCTGCCAGTGTGCAACAGACATTGCCTACGGCCCTCGTCTGTTTCGGGCAGTCCCAGCGCAGTCGCCACAACCGC

GGTGTGCGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGATACTGGCTTAACCTATGCGGCATCAGAGCAGA
5600
CCACAGCCCCGCGTCGGTACTGGGTCAGTGCATCGCTATCGCTCACATATGACCGAATTGATACGCCGTAGTCTCGTCT

NdeI
TTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAAATACCGCATCAGGCGCTCTTCC
5680
AACATGACTCTCACGTGGTATACGCCACACTTTATGGCGTGTCTACGCATTCTCTTTTATGGCGTAGTCCGCGAGAAGG

GCTTCCTCGCTCACTGACTCGCTGCGCTCGGTGCTTCGGCTGCGGGCAGCGGTATCAGCTCACTCAAAGGCGGTAATACG
5760
CGAAGGAGCGAGTGACTGAGCGACGCGAGCCAGCAAGCCGACGCCGCTCGCCATAGTCGAGTGAGTTTCCGCCATTATGC

GTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGG
5840
CAATAGGTGTCTTAGTCCCCTATTGCGTCCTTTCTTGTACACTCGTTTTCCGGTCGTTTTCCGGTCCTTGGCATTITTC

CCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGA
5920
GGCGCAACGACCGCAAAAAGGTATCCGAGGCGGGGGGACTGCTCGTAGTGTTTTAGCTGCGAGTTCAGTCTCCACCGCT

AACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCT
6000
TTGGGCTGTCTGATATTTCTATGGTCCGCAAAGGGGGACCTTCGAGGGAGCACGCGAGAGGACAAGGCTGGGACGGCGA

TACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGG
6080
ATGGCCTATGGACAGGCGGAAAGAGGGAAGCCCTTCGCACCGCGAAAGAGTATCGAGTGCGACATCCATAGAGTCAAGCC

TGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTAGCCCCGACCGCTGCGCCTTATCCGGTAACTAT
6160
ACATCCAGCAAGCGAGGTTTCGACCCGACACACGTGCTTGGGGGGCAAGTCGGGCTGGCGACGCGGAATAGGCCATTGATA

CGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTA
6240
GCAGAACTCAGGTTGGGCCATTCTGTGCTGAATAGCGGTGACCGTCGTCGGTGACCATTGTCCTAATCGTCTCGCTCCAT

TGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTC
6320
ACATCCGCCACGATGTCTCAAGAACTTCACCACCGGATTGATGCCGATGTGATCTTCTGTCATAAACCATAGACGCGAG

TGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTT
6400
ACGACTTCGGTCAATGGAAGCCTTTTTCTCAACCATCGAGAACTAGGCCGTTTGTGGTGGCGACCATCGCCACCAAAA

TTTGTGGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGC
6480
AAACAAACGTTTCGTCTCTAATGCGCGTCTTTTTTCTAGAGTTCTTCTAGGAACTAGAAAAGATGCCCCAGACTGCG

BspHI

DraI

TCAGTGGAACGAAAACACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATT
6560
AGTCACCTTGCTTTGAGTGCAATTCCTAAAACAGTACTCTAATAGTTTTCTAGAAAGTGGATCTAGGAAAATTTAA

DraI

AAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCA
6640
TTTTTACTTCAAATTTAGTTAGATTTTCAATATATACTCATTTGAACCAGACTGTCAATGGTTACGAATTAGTCACTCCGT

• Trp His Lys Ile Leu Ser Ala
AMP

CCTATCTCAGCGATCTGTCTATTTTGGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGG
6720
GGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTATCAACGGACTGAGGGGACGACATCTATTGATGCTATGCCCTCCC
Gly Ile Glu Ala Ile Gln Arg Asn Arg Glu Asp Met Thr Ala Gln Ser Gly Thr Thr Tyr Ile Val Val Ile Arg Ser Pro
AMP

CTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACC GGCTCCAGATTTATCAGCAATAAACCAGC
6800
GAATGGTAGACCGGGGTCACGACGTTACTATGGCGCTCTGGGTGCGAGTGGCCGAGGTCTAAATAGTCGTTATTTGGTCC
Lys Gly Asp Pro Gly Leu Ala Ala Ile Ile Gly Arg Ser Gly Arg Glu Gly Ala Gly Ser Lys Asp Ala Ile Phe Trp Gly
AMP

CAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCT
6880
GTCGGCCTTCCCGGCTCGCGTCTTACCAGGACGTTGAAATAGGCGGAGGTAGGTCAGATAATTAACAACGGCCCTTCGA
Ala Pro Leu Ala Ser Arg Leu Leu Pro Gly Ala Val Lys Asp Ala Glu Met Trp Asp Ile Leu Gln Gln Arg Ser Ala
AMP

FspI

PstI

AGAGTAAGTAGTTCGCCAGTTAATAGTTTGC GCAACGTTGTTGCCATTGCTGCAGGCATCGTGGTGTACGCTCGTCGTT
6960
TCTCATTCAAGCGGTCAATTATCAAACGCGTTGCAACAACGGTAACGACGTCCGTAGCACCACAGTGCGAGCAGCAA
Leu Thr Leu Leu Glu Gly Thr Leu Leu Lys Arg Leu Thr Thr Ala Met Ala Ala Pro Met Thr Thr Asp Arg Glu Asp Asn
AMP

TGGTATGGCTTCATTACGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTA
7040
ACCATACCGAAGTAAGTCGAGGCCAAGGGTTGCTAGTTCCGCTCAATGTACTAGGGGGTACAACACGTTTTTTCGCCAAT
Pro Ile Ala Glu Asn Leu Glu Pro Glu Trp Arg Asp Leu Arg Thr Val His Asp Gly Met Asn His Leu Phe Ala Thr Leu
AMP

PvuI

GCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAAT 7120
CGAGGAAGCCAGGAGGCTAGCAACAGTCTTCATTCAACCGGCGTCACAATAGTGAGTACCAATACCGTCGTGACGTATTA
Glu Lys Pro Gly Gly Ile Thr Thr Leu Leu Leu Asn Ala Ala Thr Asn Asp Ser Met Thr Ile Ala Ala Ser Cys Leu
AMP

TCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTAT 7200
AGAGAATGACAGTACGGTAGGCATTCTACGAAAAGACACTGACCACTCATGAGTTGGTTCAGTAAGACTCTTATCACATA
Glu Arg Val Thr Met Gly Asp Thr Leu His Lys Glu Thr Val Pro Ser Tyr Glu Val Leu Asp Asn Gln Ser Tyr His Ile
AMP

DraI

GCGGCGACCGAGTTGCTCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCA 7280
CGCCGCTGGCTCAACGAGAACGGGCGCAGTTGTGCCCTATTATGGCGCGGTGTATCGTCTTGAAATTTTCACGAGTAGT
Arg Arg Gly Leu Gln Glu Gln Gly Ala Asp Val Arg Ser Leu Val Ala Gly Cys Leu Leu Val Lys Phe Thr Ser Met Met
AMP

TTGGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCA 7360
AACCTTTTGCAAGAAGCCCCGCTTTTGAGAGTTCTTAGAATGGCGACAACCTCTAGGTCAAGCTACATTGGGTGAGCACGT
Pro Phe Arg Glu Glu Pro Arg Phe Ser Glu Leu Ile Lys Gly Ser Asn Leu Asp Leu Glu Ile Tyr Gly Val Arg Ala
AMP

CCCAACTGATCTTCAGCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAA 7440
GGGTTGACTAGAAGTCGTAGAAAATGAAAGTGGTCGAAAGACCCACTCGTTTTTGTCTTCCGTTTACGGCGTTTTTT
Gly Leu Gln Asp Glu Ala Asp Lys Val Lys Val Leu Thr Glu Pro His Ala Phe Val Pro Leu Cys Phe Ala Ala Phe Phe
AMP

GGGAATAAGGGCGACACGGAATGTTGAATACTCATCTCTTCTTTTCAATATTATTGAAGCATTTATCAGGGTTATT 7520
CCCTTATTTCCGCTGTGCCTTTACAACCTATGAGTATGAGAAGGAAAAAGTTATAATACTTCGTAAATAGTCCCAATAA
Pro Ile Leu Ala Val Arg Phe His Gln Ile Ser Met
AMP

BspHI

GTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTG 7600
CAGAGTACTCGCCTATGTATAAAGTTACATAAATCTTTTATTTGTTTATCCCAAGGCGCGTGTAAGGGGCTTTTTCAC

BspHI

CCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTTCGTCTTCA 7680
GGTGGACTGCAGATTCTTTGGTAATAATAGTACTGTAATTGGATATTTTATCCGCATAGTGCTCCGGGAAAGCAGAAGT

AGAAT
→ 7685
TCTTA

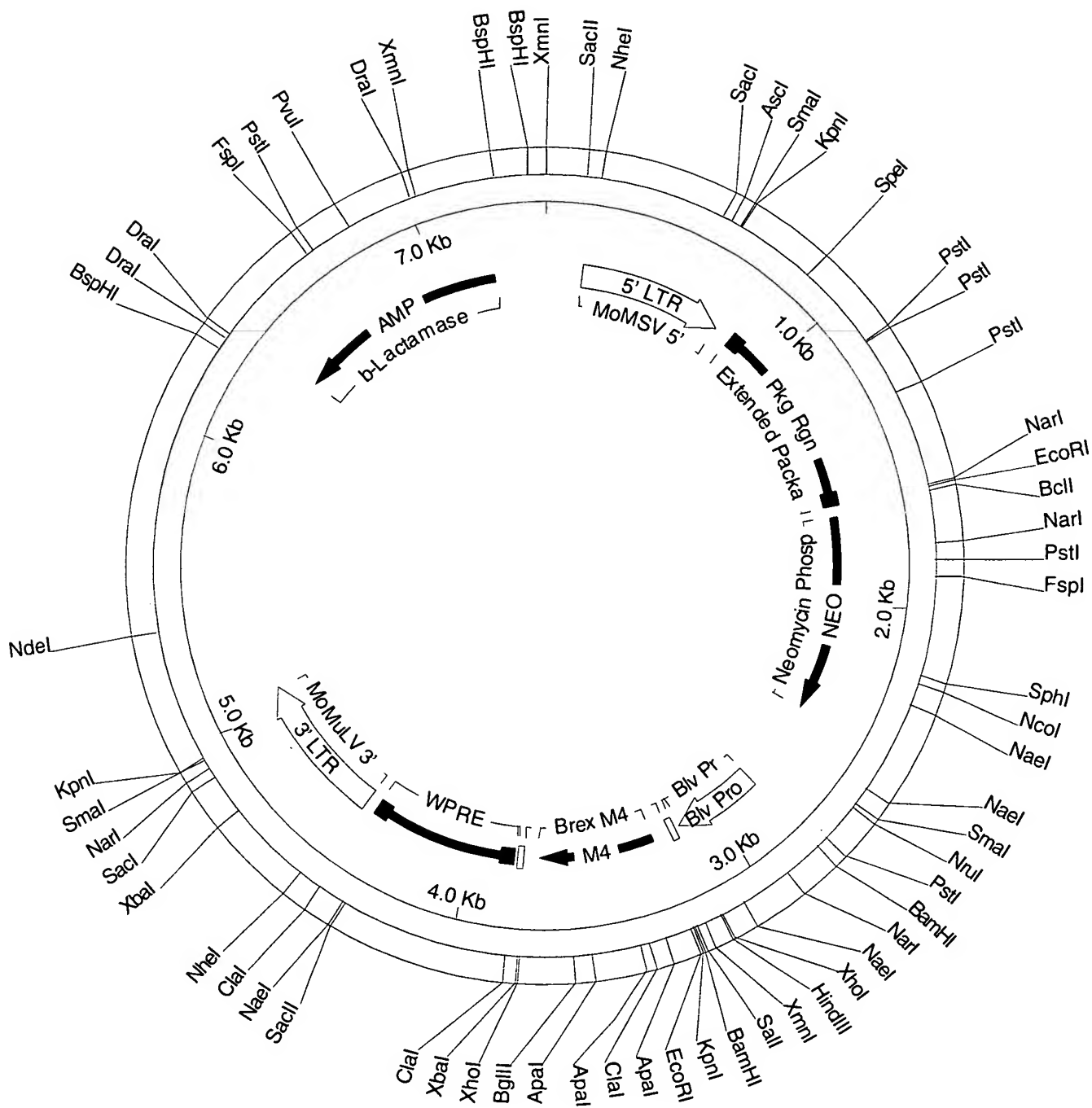


FIG. 11

FIG. 12

Page 1

Thursday, June 13, 2002 3:55 PM

GD2415 (pLNBlv-M4W).MPD (1 > 7428) Site and Sequence

Enzymes : 35 of 538 enzymes (Filtered)

Settings : Circular, Certain Sites Only, Standard Genetic Code

XmnI

GAATTAATTCATACCAGATACCCGAAAACGTGCTCCAAATGTGTCCCCCTCACACTCCCAAATTCGCGGGCTTCTGCCT
CTTAATTAAGTATGGTCTAGTGGCTTTTGACAGGAGGTTTACACAGGGGGAGTGTGAGGGTTTAAGCGCCCGAAGACGGA

SacII

CTTAGACCACTCTACCCTATTCCTCCACACTCACCGGAGCCAAAGCCGCGCCCTTCCGTTTCTTTGCTTTTGAAAGACCC
GAATCTGGTGAGATGGGATAAGGGGTGTGAGTGGCTCGGTTTCGGCGCCGGGAAGGCAAAGAAACGAAAACCTTCTGGG

5' LTR

MoMSV 5' LTR

NheI

CACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTC
GTGGGCATCCACCGTTTCGATCGAATTCATTGCGGTGAAACGTTCCGTACCTTTTTATGTATTGACTCTTATCTTTTCAAG

5' LTR

MoMSV 5' LTR

AGATCAAGGTCAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGCGGTTCTTGCCCCGGCTCAGGGC
TCTAGTTCAGTCTTGTCTTTGTCGACTTATGGTTTGCTCTATAGACACCATTCGCCAAGGACGGGGCCGAGTCCCG

5' LTR

MoMSV 5' LTR

CAAGAACAGATGAGACAGCTGAGTGATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTTGCCCCGGCTCGGGGCCAAG
GTTCTTGCTACTCTGTGACTCACTACCCGGTTTGCTCTATAGACACCATTCGTCAAGGACGGGGCCGAGCCCCGGTTC

5' LTR

MoMSV 5' LTR

AACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATCATCAGATGTTTCCAGGGTGCCCCAAGGACC
TTGTCTACCAGGGGTCTACGCCAGGTGCGGAGTCGTCAAAGATCACTAGTAGTCTACAAAGGTCCCACGGGGTTCTGG

5' LTR

MoMSV 5' LTR

TGAAAATGACCCTGTACCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCCGCTCTCCGAGC
ACTTTTACTGGGACATGGAATAAACTTGATTGGTTAGTCAAGCGAAGAGCGAAGACAAGCGCGCGAAGGCGAGAGGCTCG

5' LTR

MoMSV 5' LTR

SacI

Ascl

SmaI

KpnI

TCAATAAAAGAGCCCAACAACCCCTCACTCGGCGCGCCAGTCTTCCGATAGACTGCGTCGCCCCGGGTACCCGTATTCCCAA
AGTTATTTTCTCGGGTGTGGGGAGTGAGCCGCGCGGTGAGAAGGCTATCTGACGCAGCGGGCCCATGGGCATAAGGGTT

5' LTR

MoMSV 5' LTR

FIG. 12 (cont)

Thursday, June 13, 2002 3:55 PM

GD2415 (pLNBlv-M4W).MPD (1 > 7428) Site and Sequence

Page 2

TAAAGCCTCTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCCCTGGGAGGGTCTCCTCTGAGTGATTGACTACCCAC 720
ATTCGGAGAACGACAAACGTAGGCTTAGCACCAGAGCGACAAGGAACCTCCCAGAGGAGACTCACTAACTGATGGGTG
5' LTR
MoMSV 5' LTR

GACGGGGTCTTTTCATTTGGGGGCTCGTCCGGGATTTGGAGACCCCTGCCAGGGACCACCGACCCACCACCGGGAGGTA 800
CTGCCCCCAGAAAGTAAACCCCCGAGCAGGCCCTAAACCTCTGGGGACGGGTCCCTGGTGGCTGGGTGGTGGCCCTCCAT
5' LTR
MoMSV 5' LTR

AGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTGATGTTATGCGCCTGCGTCTGTACTAGTT 880
TCGACCGGTGCGTTGAATAGACACAGACAGGCTAACAGATCACAGATACAACTACAATACGGGACGCAGACATGATCAA
Pkg Rgn
Extended Packaging Region

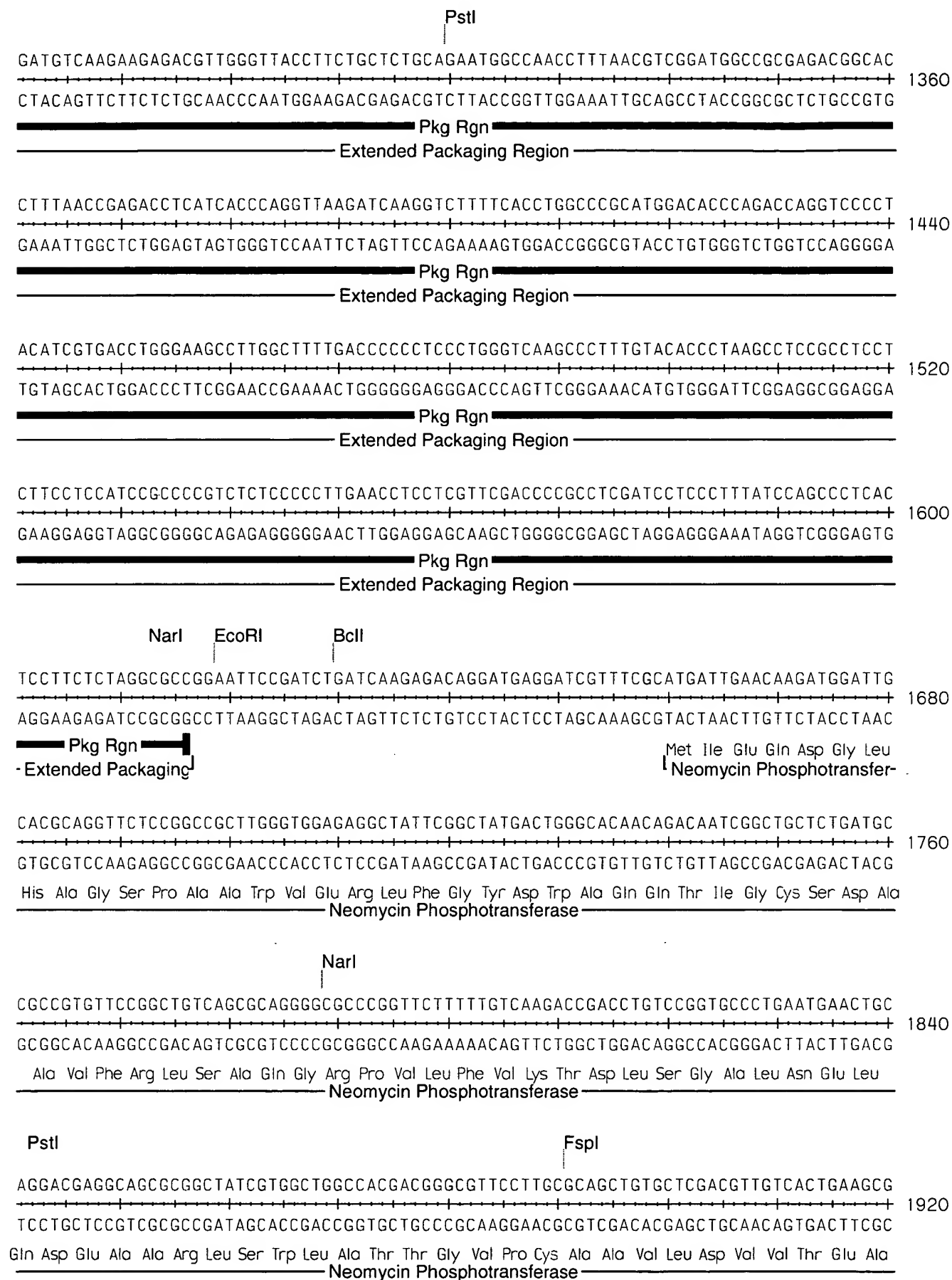
AGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACCCCTGGGAGACGTC 960
TCGATTGATCGAGACATAGACCGCTGGGCACCACCTTGACTGTCTAAGACTTGTGGGCCGGCGTTGGGACCCCTCTGCAG
Pkg Rgn
Extended Packaging Region

CCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTG 1040
GGTCCCTGAAACCCCGGCAAAAACACCGGGCTGGACTCCTTCCCTCAGCTACACCTTAGGCTGGGGCAGTCCTATACAC
Pkg Rgn
Extended Packaging Region

GTTCTGGTAGGAGACGAGAACCTAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTTCGGTTTGAACCGAAGCCGCGC 1120
CAAGACCATCCTCTGCTCTTGATTTTGTCAAGGGCGGAGGCAGACTTAAAAACGAAAGCCAAACCTTGGCTTCGGCGCG
Pkg Rgn
Extended Packaging Region

PstI PstI
GTCTTGCTGCTGCAGCGCTGCAGCATCGTTCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGG 1200
CAGAACAGACGACGTCGCGACGTCGTAGCAAGACACAACAGAGACAGACTGACACAAAGACATAAACAGACTTTTAATCC
Pkg Rgn
Extended Packaging Region

GCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAACCAAGTCGGTA 1280
CGGTCTGACAAATGGTGAGGGAATTCAAACCTGGAATCCAGTGACCTTTCTACAGCTCGCCTAGCGAGTGTGGTCAGCCAT
Pkg Rgn
Extended Packaging Region



GGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATC
 CTTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAG
 Gly Arg Asp Trp Leu Leu Leu Gly Glu Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys Val Ser
 Neomycin Phosphotransferase

CATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCA
 GTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAAGCTGGTGGTTTCGCTTTGTAGCGT
 Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg
 Neomycin Phosphotransferase

TCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCA
 AGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGT
 Ile Glu Arg Ala Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu Glu His Gln Gly Leu Ala Pro
 Neomycin Phosphotransferase

GCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCC
 CGGCTTGACAAGCGGTCCGAGTTCGCGCGGTACGGGTGCCGCTCTAGAGCAGCACTGGGTACCGCTACGGACGAACGG
 Ala Glu Leu Phe Ala Arg Leu Lys Ala Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys Leu Pro
 SphI NcoI
 Neomycin Phosphotransferase

GAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTTCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACA
 CTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCTGT
 Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp
 NaeI
 Neomycin Phosphotransferase

TAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCC
 ATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGG
 Ile Ala Leu Ala Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe Leu Val Leu Tyr Gly Ile Ala
 Neomycin Phosphotransferase

GCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTGAAATGACC
 CGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGG
 Ala Pro Asp Ser Gln Arg Ile Ala Phe Tyr Arg Leu Leu Asp Glu Phe Phe
 Neomycin Phosphotransferase

GACCAAGCGACGCCAACCTGCCATCACGAGATTTGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCGT
 CTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCA

TTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGATCTCATGCTGGAGTTCTTCGCCACCCCGGGCTCGATCCCC
 AAAGGCCCTGCGGCCGACCTACTAGGAGGTGCGGCCCTAGAGTACGACCTCAAGAAGCGGTGGGGCCCGAGCTAGGGG
 NaeI SmaI

NruI

TCGCGAGTTGGTTTCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGCAAATCCGTCGGCATCCAG 2720
AGCGCTCAACCAAGTCGACGACGGAAGTCCGACCTGCTGGAGCGCCTCAAGATGGCCGTACGTTTAGGCAGCCGTAGGTC

PstI

GAAACCAGCAGCGGCTATCCGCGCATCCATGCCCCGAAGTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAGGC 2800
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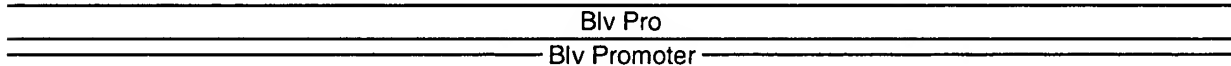
BamHI

GGATCCTAGCAGAAAAATAAGACTTGATTCCCCCTTAAATACAACTGCTAGAAAATGAATGGCTCTCCCGCTTTTTT 2880
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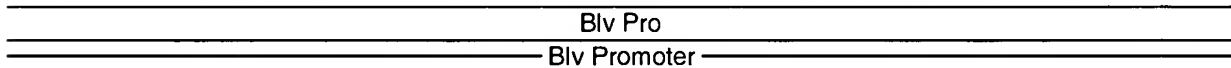


NarI

GAGGGGGAATCATTGTATGAAAGATCATGCCGACCTAGGCGCCGCCACCGCCCCGTAAACCAGACAGAGACGTACGCTG 2960
CTCCCCCTTAGTAAACATACTTTCTAGTACGGCTGGATCCGCGGCGGTGGCGGGGCATTTGGTCTGTCTCTGCAGTCGAC



CCAGAAAAGCTGGTGACGGCAGCTGGTGGCTAGAATCCCCGTACCTCCCCAACTTCCCCTTTCCCGAAAAATCCACACCC 3040
GGTCTTTTCGACCACTGCCGTCGACCACCGATCTTAGGGGCATGGAGGGGTGAAGGGGAAAGGGCTTTTAGGTGTGGG



NaeI

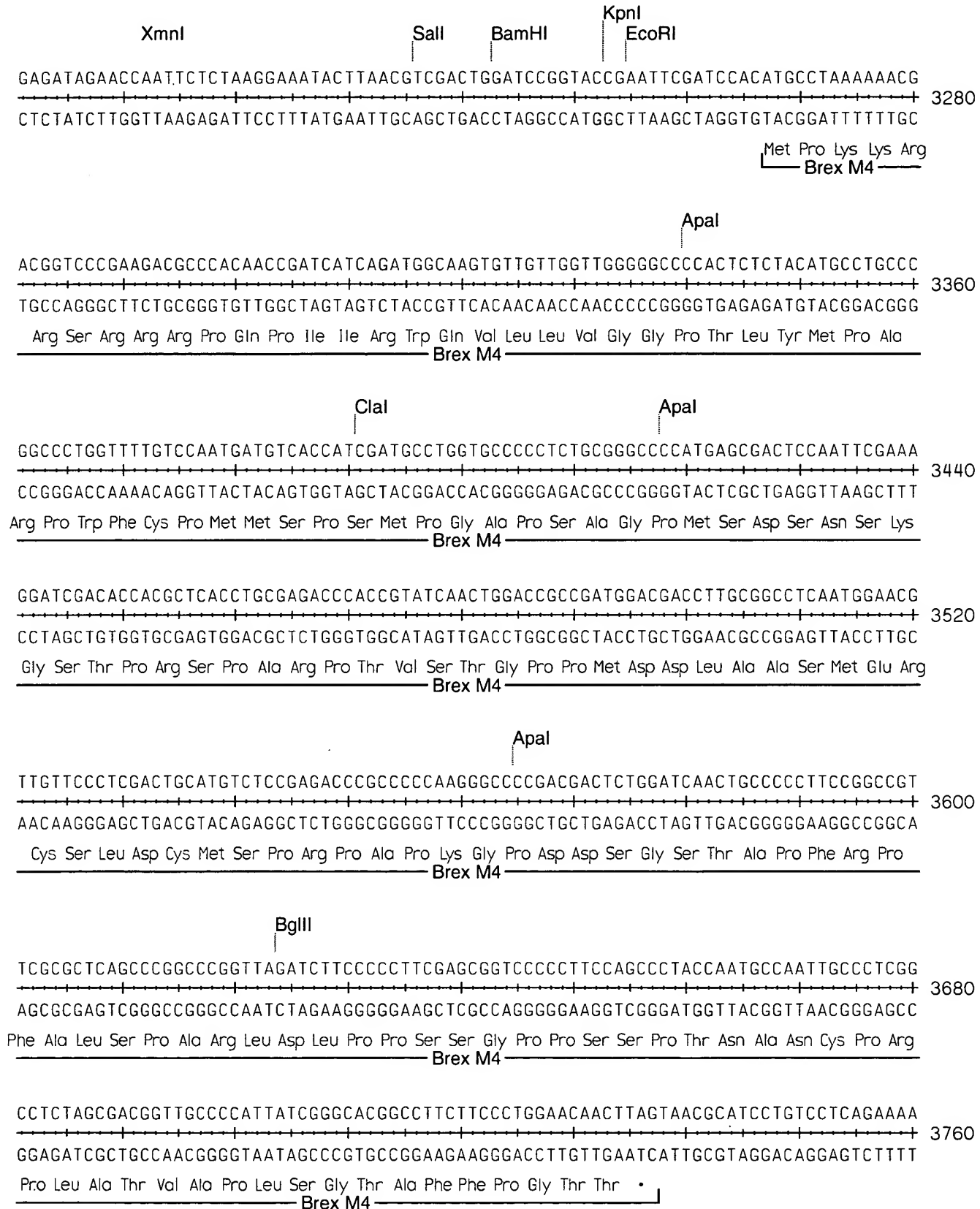
TGAGCTGCTGACCTCACCTGCTGATAAATTAATAAAATGCCGGCCCTGTGAGTTAGCGGCACCAGAAGCGTTCTTCTCC 3120
ACTCGACGACTGGAGTGGACGACTATTTAATTATTTACGGCCGGGACAGCTCAATCGCCGTGGTCTTCGCAAGAAGAGG

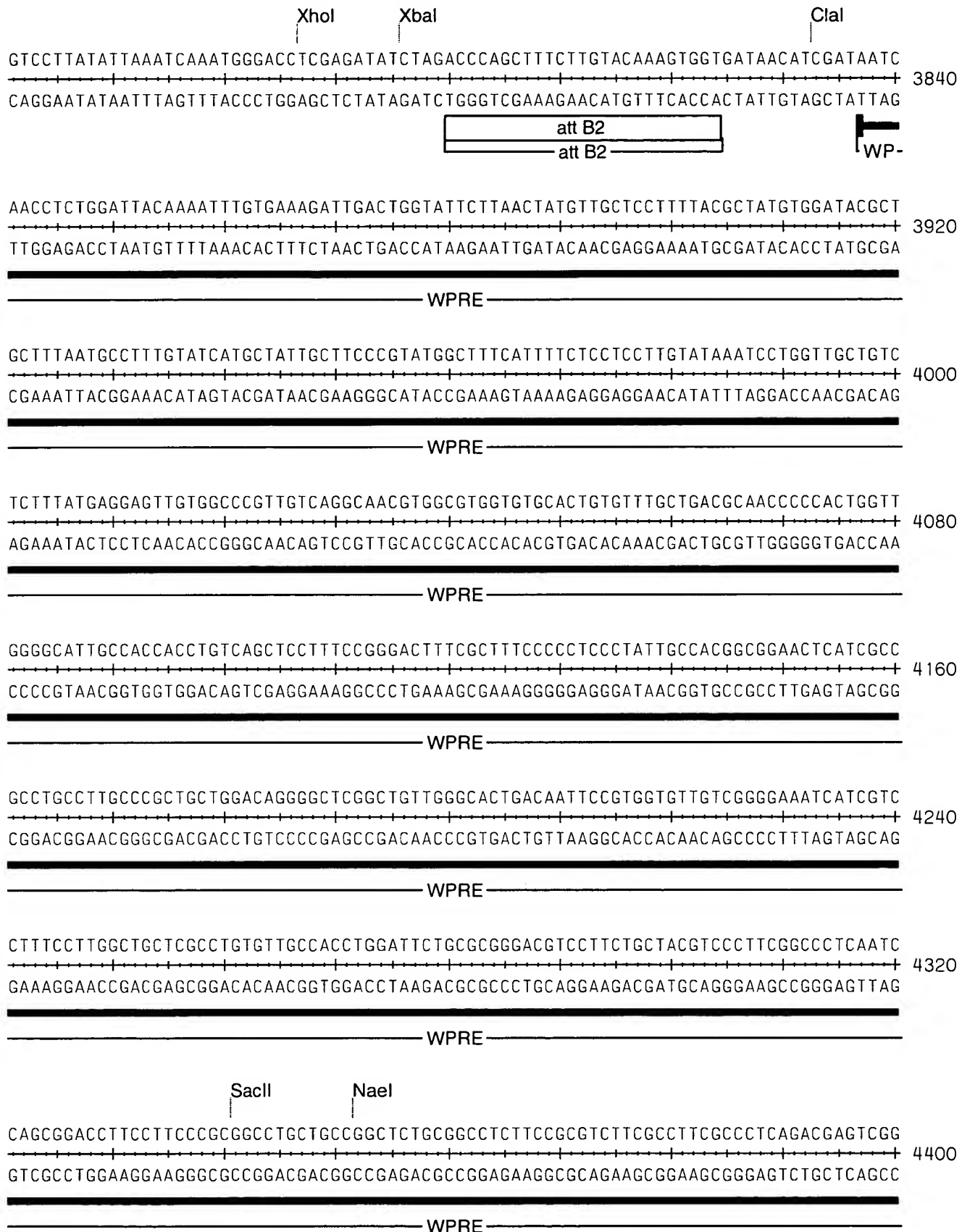


XhoI HindIII

TGAGACCCTCGTGCTCAGCTCTCGGTCTGCTCGAGAAGCTTGTTATCACAAGTTTGTACAAAAAGCAGGCTTCAAG 3200
ACTCTGGGAGCAGAGTCGAGAGCCAGGACGGAGCTCTTCAACAATAGTGTTCAAACATGTTTTTCGTCCGAAGCTTC







Thursday, June 13, 2002 3:55 PM
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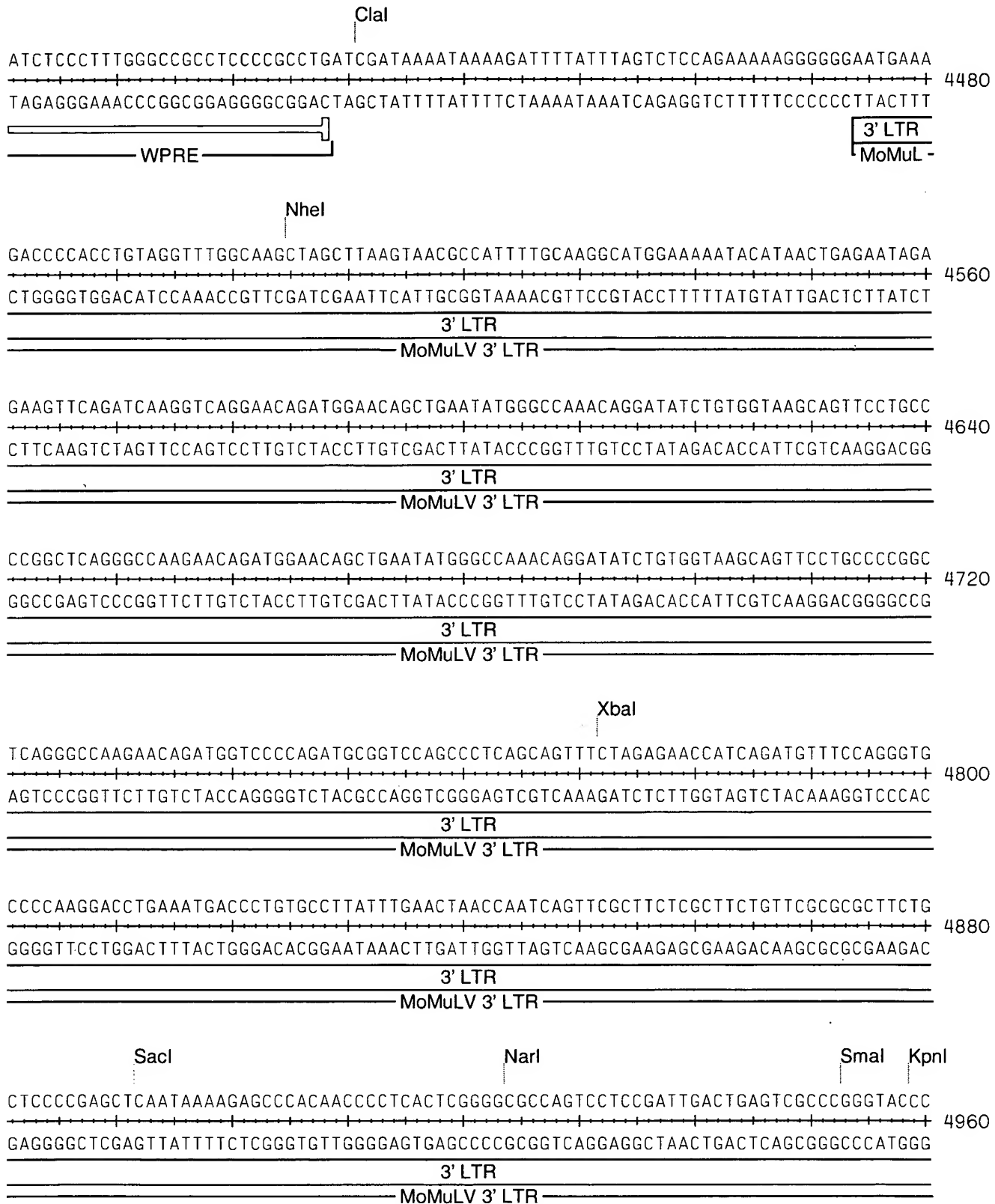


FIG. 12 (cont)

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GD2415 (pLNBiv-M4W).MPD (1 > 7428) Site and Sequence

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CACATAGGTTATTTGGGAGAACGTCAACGTAGGCTGAACACCAGAGCGACAAGGAACCTCCCAGAGGAGACTCACTAAC
3' LTR
MoMuLV 3' LTR

ACTACCGTCAGCGGGGTCTTTCATTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCAGGGACCACCGACCCACCA 5120
TGATGGGCAGTCGCCCCAGAAAGTAAACCCCCGAGCAGGCCCTAGCCCTCTGGGGACGGGTCCCTGGTGGCTGGGTGGT
3' LTR
MoMuLV 3' LTR

CCGGGAGGTAAGCTGGCTGCCTCGCGGTTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTC 5200
GGCCCTCCATTGACCGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGGAGACTGTGTACGTCGAGGGCCTCTGCCAG

ACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCGGGTGTGGGGCGC 5280
TGTCGAACAGACATTGCCTACGGCCCTCGTCTGTTTCGGGCAGTCCCGCGCAGTCGCCACAACCGCCACAGCCCCGCG

AGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATACTGGCTTAACTATGCGGCATCAGAGCAGATTGTAAGTACTGAGAGT 5360
TCGGTACTGGGTCAGTGCATCGCTATCGCCTCACATATGACCGAATTGATACGCCGTAGTCTCGTCTAACATGACTCTCA

NdeI

GCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCTCTTCCGCTTCTCGCTCA 5440
CGTGGTATACGCCACACTTTATGGCGTGTCTACGCATTCTCTTTTATGGCGTAGTCCGCGAGAAGGCGAAGGAGCGAGT

CTGACTCGCTGCGCTCGGTCTGCTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAA 5520
GACTGAGCGACGCGAGCCAGCAAGCCGACGCCGCTCGCCATAGTCGAGTGAGTTTCCGCCATTATGCCAATAGGTGTCTT

TCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGC 5600
AGTCCCCTATTGCGTCTTTCTTGTACACTCGTTTTCCGGTCGTTTTCCGGTCCTTGGCATTCTTCCGGCGCAACGACCG

GTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGAC 5680
CAAAAAGGTATCCGAGGCGGGGGGACTGCTCGTAGTGTTTTAGCTGCGAGTTCAGTCTCCACCGCTTGGGCTGTCTTG

TATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTG 5760
ATATTTCTATGGTCCGCAAAGGGGGACCTTCGAGGGAGCACGCGAGAGGACAAGGCTGGGACGGCGAATGGCCTATGGAC

TCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCTG 5840
AGGCGGAAAGAGGGAAGCCCTTCGCACCGCGAAAGAGTATCGAGTGCGACATCCATAGAGTCAAGCCACATCCAGCAAGC

CTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCA 5920
GAGGTTTCGACCCGACACACGTGCTTGGGGGGCAAGTCGGCTGGCGACGCGGAATAGGCCATTGATAGCAGAACTCAGGT

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GD2415 (pLNBlv-M4W).MPD (1 > 7428) Site and Sequence

ACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCT
 TGGGCCATTCTGTGCTGAATAGCGGTGACCGTCGTCGGTGACCATTTGCCTAATCGTCTCGCTCCATACATCCGCCACGA 6000

ACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGT
 TGTCTCAAGAACTTCACCACCGGATTGATGCCGATGTGATCTTCTGTGTCATAAACCATAGACGCGAGACGACTTCGGTCA 6080

TACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTITGCAAGC
 ATGGAAGCCTTTTTCTCAACCATCGAGAACTAGGCCGTTTGTITGGTGCGGACCATCGCCACCAAAAAACAAACGTTTCG 6160

AGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAA
 TCGTCTAATGCGCGTCTTTTTTCTAGAGTTCTTCTAGGAACTAGAAAAGATGCCCCAGACTGCGAGTCACCTTGCTT 6240

BspHI

DraI

AACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTT
 TTGAGTGCAATTCCTTAAACAGTACTCTAATAGTTTTTCTAGAAAGTGGATCTAGGAAAATTTAATTTTACTTCAAA 6320

DraI

TAAATCAATCTAAAGTATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGA
 ATTTAGTTAGATTTTCATATATACTCATTGAACCAGACTGTCAATGGTTACGAATTAGTCACTCCGTGGATAGAGTCGCT 6400

• Trp His Lys Ile Leu Ser Ala Gly Ile Glu Ala Ile
 b-Lactamase

TCTGTCTATTTCTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGC
 AGACAGATAAAGCAAGTAGGTATCAACGGACTGAGGGGCAGCACATCTATTGATGCTATGCCCTCCGAATGGTAGACCG 6480

Gln Arg Asn Arg Glu Asp Met Thr Ala Gln Ser Gly Thr Thr Tyr Ile Val Val Ile Arg Ser Pro Lys Gly Asp Pro
 b-Lactamase

CCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACC GGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGAAGGGC
 GGGTCACGACGTTACTATGGCGCTCTGGGTGCGAGTGCCGAGGTCTAAATAGTCGTTATTTGGTCGGTCGGCCTTCCCG 6560

Gly Leu Ala Ala Ile Ile Gly Arg Ser Gly Arg Glu Gly Ala Gly Ser Lys Asp Ala Ile Phe Trp Gly Ala Pro Leu Ala
 b-Lactamase

CGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGTAAGTAGTT
 GCTCGCGTCTTACCAGGACGTTGAAATAGGCGGAGGTAGGTCAGATAATTAACAACGGCCCTTCGATCTCATTATCAAA 6640

Ser Arg Leu Leu Pro Gly Ala Val Lys Asp Ala Glu Met Trp Asp Ile Leu Gln Gln Arg Ser Ala Leu Thr Leu Leu Glu
 b-Lactamase

FspI

PstI

CGCCAGTTAATAGTTTGC GCAACGTTGTTGCCATTGCTGCAGGCATCGTGGTGTACGCTCGTCGTTTGGTATGGCTTCA
 GCGGTCAATTATCAAACGCGTTGCAACAACGGTAACGACGTCCGTAGCACCACAGTGCGAGCAGCAAACCATACCGAAGT 6720

Gly Thr Leu Leu Lys Arg Leu Thr Thr Ala Met Ala Ala Pro Met Thr Thr Asp Arg Glu Asp Asn Pro Ile Ala Glu
 b-Lactamase

TTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCC 6800
 AAGTCGAGGCCAAGGGTTGCTAGTTCCGCTCAATGTACTAGGGGTACAACACGTTTTTTCGCCAATCGAGGAAGCCAGG
 Asn Leu Glu Pro Glu Trp Arg Asp Leu Arg Thr Val His Asp Gly Met Asn His Leu Phe Ala Thr Leu Glu Lys Pro Gly
 b-Lactamase

PvuI

TCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCA 6880
 AGGCTAGCAACAGTCTTCATTCAACCGGCGTCACAATAGTGAGTACCAATACCGTCGTGACGTATTAAGAGAATGACAGT
 Gly Ile Thr Thr Leu Leu Leu Asn Ala Ala Thr Asn Asp Ser Met Thr Ile Ala Ala Ser Cys Leu Glu Arg Val Thr Met
 b-Lactamase

TGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGATGCGGCGACCGAGT 6960
 ACGGTAGGCATTCTACGAAAAGACACTGACCACTCATGAGTTGGTTCAGTAAGACTCTTATCACATACGCCGCTGGCTCA
 Gly Asp Thr Leu His Lys Glu Thr Val Pro Ser Tyr Glu Val Leu Asp Asn Gln Ser Tyr His Ile Arg Arg Gly Leu
 b-Lactamase

DraI

XmnI

TGCTCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTT 7040
 ACGAGAACGGGCGCAGTTGTGCCCTATTATGGCGCGGTGTATCGTCTTGAAATTTTACGAGTAGTAACCTTTTGCAAG
 Gln Glu Gln Gly Ala Asp Val Arg Ser Leu Val Ala Gly Cys Leu Leu Val Lys Phe Thr Ser Met Met Pro Phe Arg Glu
 b-Lactamase

TTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTTCGATGTAACCCACTCGTGACCCAACTGATCTT 7120
 AAGCCCCGCTTTTGAGAGTTCCCTAGAATGGCGACAACCTCTAGGTCAAGCTACATTGGGTGAGCACGTGGGTTGACTAGAA
 Glu Pro Arg Phe Ser Glu Leu Ile Lys Gly Ser Asn Leu Asp Leu Glu Ile Tyr Gly Val Arg Ala Gly Leu Gln Asp Glu
 b-Lactamase

CAGCATCTTTTACTTTACCCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGGCG 7200
 GTCGTAGAAAATGAAAGTGGTCGAAAGACCCACTCGTTTTTGTCTTCCGTTTTACGGCGTTTTTCCCTTATTCCCGC
 Ala-Asp Lys Val Lys Val Leu Thr Glu Pro His Ala Phe Val Pro Leu Cys Phe Ala Ala Phe Phe Pro Ile Leu Ala
 b-Lactamase

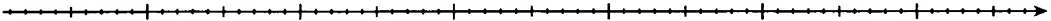
BspHI

ACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGG 7280
 TGTGCCCTTACAACCTTATGAGTATGAGAAGGAAAAAGTTATAATAACTTCGTAAATAGTCCCAATAACAGAGTACTCGCC
 Val Arg Phe His Gln Ile Ser Met
 b-Lactamase

ATACATATTTGAATGTATTTAGAAAAATAACAAATAGGGGTTCCGCGCACATTTCCCGAAAAGTGCCACCTGACGTCT 7360
 TATGTATAAACTTACATAAATCTTTTTATTTGTTTATCCCAAGGCGCGTGTAAAGGGGCTTTTCACGGTGGACTGCAGA

BspHI

AAGAAACCATTATTATCATGACATTAACTATAAAAAATAGGCGTATCACGAGGCCCTTTCGTCTTCAA
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7428

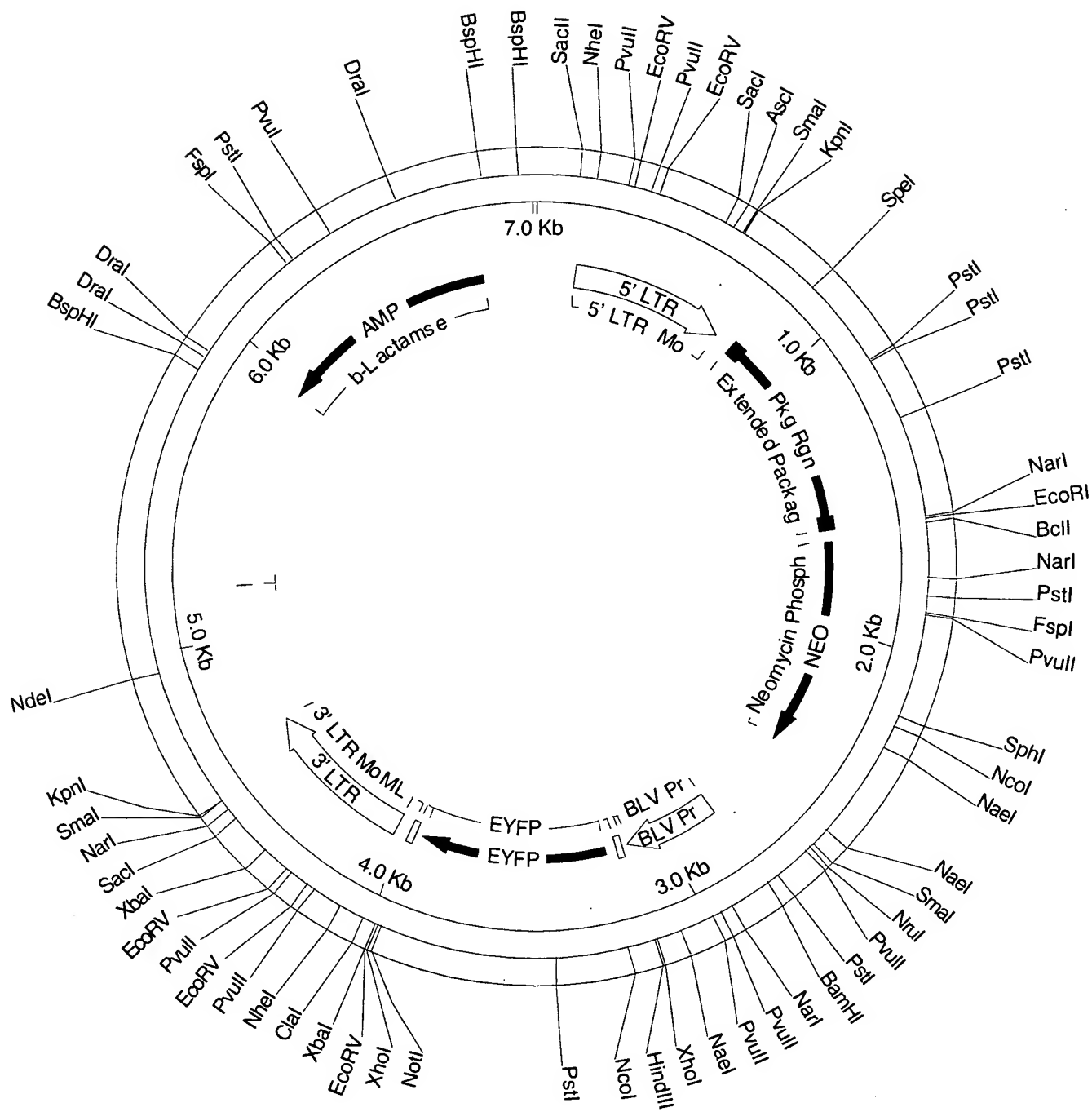


FIG. 13

FIG. 14

Page 1

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GD2407 pLNBLV-YFP Map.MPD (1 > 7010) Site and Sequence

Enzymes : 36 of 538 enzymes (Filtered)

Settings : Circular, Certain Sites Only, Standard Genetic Code

GAATTAATTCATACCAGATCACCGAAAACGTGCTCTCAAATGTGTCCCTCACACTCCCAAATTCGCGGGCTTCTGCCT
CTTAATTAAGTATGGTCTAGTGGCTTTTGACAGGAGGTTTACACAGGGGAGTGTGAGGGTTTAAGCGCCGAAGACGGA

SacII

CTTAGACCACTCTACCCTATTCCCCACACTCACCGGAGCCAAAGCCGCGGCCCTTCCGTTTCTTTGCTTTTGAAAGACCC
GAATCTGGTGAGATGGGATAAGGGGTGTGAGTGGCTTCGGTTTCGGCGCCGGAAGGCAAAGAAACGAAAACTTTCTGGG

5' LTR

5' LTR MoMS-

NheI

CACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTC
GTGGGCATCCACCGTTCGATCGAATTCATTGCGGTGAAACGTTCCGTACCTTTTATGTATTGACTCTTATCTTTTCAAG

5' LTR

5' LTR MoMSV

PvuII

EcoRV

AGATCAAGGTCAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGCGGTTCTTGCCCCGGCTCAGGGC
TCTAGTTCCAGTCCTTGTTTCTTTGTGCACTTATGGTTTGTCTATAGACACCATTCGCCAAGGACGGGGCCGAGTCCCG

5' LTR

5' LTR MoMSV

PvuII

EcoRV

CAAGAACAGATGAGACAGCTGAGTGATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTTGCCCCGGCTCGGGGCCAAG
GTTCTTGTCTACTCTGTGCACTCACTACCCGGTTTGTCTATAGACACCATTCGTCAGGACGGGGCCGAGCCCCGGTTC

5' LTR

5' LTR MoMSV

AACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATCATCAGATGTTTCCAGGGTGCCCCAAGGACC
TTGTCTACCAGGGGTCTACGCCAGGTGCGGAGTCGTCAAAGATCACTTAGTAGTCTACAAAGGTCCACGGGGTTCTCTGG

5' LTR

5' LTR MoMSV

TGAAAATGACCCTGTACCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCCGCTCTCCGAGC
ACTTTTACTGGGACATGGAATAAACTTGATTGGTTAGTCAAGCGAAGAGCGAAGACAAGCGCGCGAAGGCGAGAGGCTCG

5' LTR

5' LTR MoMSV

FIG. 14 (cont)

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GD2407 pLNBLV-YFP Map.MPD (1 > 7010) Site and Sequence

GCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCAGTGGAAAGATGTCGAGCGGATCGCTCACAACCAGTCGGTA
 CGGTCTGACAATGGTGAGGGAATTCAAACCTGGAATCCAGTGACCTTCTACAGCTCGCCTAGCGAGTGTGGTCAGCCAT
 Pkg Rgn
 Extended Packaging Region

GATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTGGATGGCCGCGAGACGGCAC
 CTACAGTTCTTCTCTGCAACCCAATGGAAGACGAGACGTCTTACCGGTTGAAATTGCAGCCTACCGGCGCTCTGCCGTG
 Pkg Rgn
 Extended Packaging Region

CTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTCTTTTACCTGGCCCGCATGGACACCCAGACCAGGTCCCT
 GAAATTGGCTCTGGAGTAGTGGGTCCAATTCTAGTTCCAGAAAAGTGGACCGGGCGTACCTGTGGGTCTGGTCCAGGGGA
 Pkg Rgn
 Extended Packaging Region

ACATCGTGACCTGGGAAGCCTTGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAGCCTCCGCCTCT
 TGTAGCACTGGACCTTCGGAACCGAAAACCTGGGGGGAGGGACCCAGTTCCGGGAAACATGTGGGATTCCGAGGCGGAGGA
 Pkg Rgn
 Extended Packaging Region

CTTCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCAC
 GAAGGAGGTAGGCGGGCAGAGAGGGGGAACCTTGGAGGAGCAAGCTGGGGCGGAGCTAGGAGGGAAATAGGTCGGGAGTG
 Pkg Rgn
 Extended Packaging Region

NarI EcoRI BclI
 TCCTTCTCTAGGCGCCGAATTCCGATCTGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTG
 AGGAAGAGATCCGCGGCCTTAAGGCTAGACTAGTTCTCTGTCTACTCCTAGCAAAGCGTACTAAGTTGTTCTACCTAAC
 Pkg Rgn
 Extended Packaging
 Met Ile Glu Gln Asp Gly Leu
 Neomycin Phosphotransferase

CACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCCGGCTATGACTGGGCACAACAGACAATCCGGCTGCTCTGATGC
 GTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACG
 His Ala Gly Ser Pro Ala Ala Trp Val Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser Asp Ala
 Neomycin Phosphotransferase

NarI
 CGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGC
 GCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACG
 Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu
 Neomycin Phosphotransferase



FIG. 14 (cont)

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GD2407 pLNBLV-YFP Map.MPD (1 > 7010) Site and Sequence

GACCAAGCGACGCCAACCTGCCATCACGAGATTTGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCGT 2560
CTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCA

NaeI

SmaI

TTTCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCGGGCTCGATCCCC 2640
AAAGGCCCTGCGGCCGACCTACTAGGAGGTGCGCCCCCTAGAGTACGACCTCAAGAAGCGGTGGGGCCCCGAGCTAGGGG

NruI

PvuII

TCGCGAGTTGGTTCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGCAAATCCGTCGGCATCCAG 2720
AGCGCTCAACCAAGTCGACGACGGACTCCGACCTGCTGGAGCGCTCAAGATGGCCGTACGTTTAGGCAGCCGTAGGTC

PstI

GAAACCAGCAGCGGCTATCCGCGCATCCATGCCCCGAACGTCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAGGC 2800
CTTTGGTCGTCGCCGATAGCGCGTAGGTACGGGGGCTTGACGTCTCACCCCTCCGTGCTACCGGCGAAACCAGTCCG

BamHI

GGATCCTAGCAGAAAAATAAGACTTGATTCCCCCTTAAATACAACTGCTAGAAAATGAATGGCTCTCCCGCCTTTTTT 2880
CCTAGGATCGTCTTTTTATTCTGAACCTAAGGGGGAATTTAATGTTGACGATCTTTTACTTACCGAGAGGGCGGAAAAAA

BLV Pro

BLV Promoter

NarI

PvuII

GAGGGGAATCATTTGTATGAAAGATCATGCCGACCTAGGCGCCGCCACCGCCCCGTAAACCAGACAGAGACGTACGCTG 2960
CTCCCCCTTAGTAAACATACTTTCTAGTACGGCTGGATCCGCGCGGTTGGCGGGGCATTTGGTCTGTCTCTGCAGTCGAC

BLV Pro

BLV Promoter

PvuII

CCAGAAAAGCTGGTGACGGCAGCTGGTGGCTAGAATCCCCGTACCTCCCCAACTTCCCCTTTCCCGAAAAATCCACACCC 3040
GGTCTTTTCGACCACTGCCGTCGACCACCGATCTTAGGGGCATGGAGGGGTTGAAGGGGAAAGGGCTTTTTAGGTGTGGG

BLV Pro

BLV Promoter

NaeI

TGAGCTGCTGACCTCACCTGCTGATAAATTAATAAAATGCCGGCCCTGTGAGTTAGCGGCACCAGAAGCGTTCTTCTCC 3120
ACTCGACGACTGGAGTGGACGACTATTTAATTATTTACGGCCGGGACAGCTCAATCGCCGTGGTCTTCGCAAGAAGAGG

BLV Pro

BLV Promoter

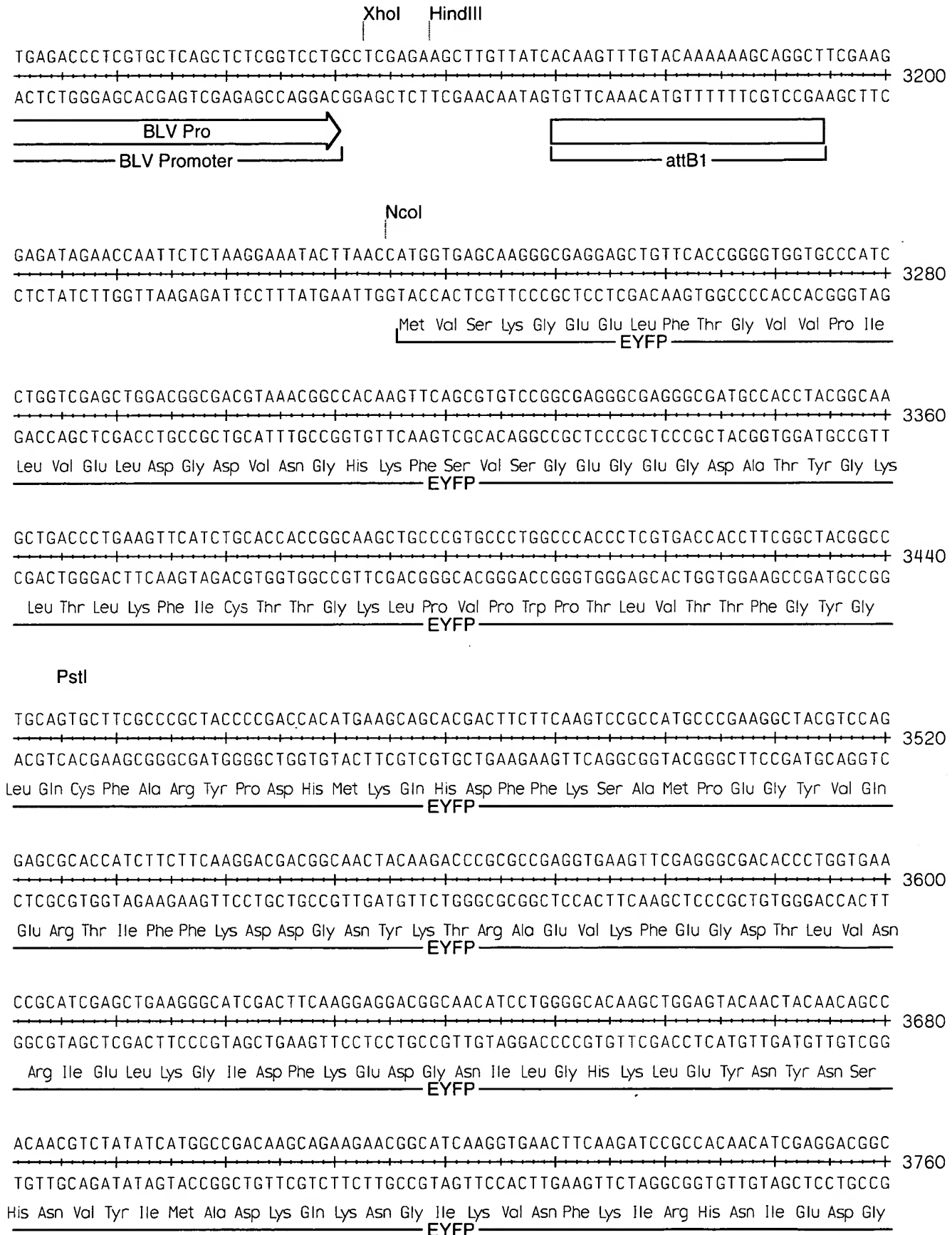


FIG. 14 (cont)

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GD2407 pLNBLV-YFP Map.MPD (1 > 7010) Site and Sequence

AGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCACAACCACTACCT
 TCGCACGTCGAGCGGCTGGTGATGGTCGTCTTGTGGGGGTAGCCGCTGCCGGGGCACGACGACGGGCTGTTGGTGATGGA
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
 EYFP

GAGCTACCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTCTGCTGGAGTTCGTGACCGCCGCCG
 CTCGATGGTCAGGCGGGACTCGTTTCTGGGGTTGCTCTTCGCGCTAGTGTACCAGGACGACCTCAAGCACTGGCGGGCGG
 Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
 EYFP

GGATCACTCTCGGCATGGACGAGCTGTACAAGTAAAGCGGCCGCACTCGAGATATCTAGACCCAGCTTTCTTGTACAAAG
 CCTAGTGAGAGCCGTACCTGCTCGACATGTTCAATTCGCCGGCGTGAGCTCTATAGATCTGGGTCGAAAGAACATGTTTC
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 EYFP attB2
 attB2

Clal
 TGGTGATAACATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCACCTGTAGGTTT
 ACCACTATTGTAGCTATTTTATTTTCTAAAATAAATCAGAGGTCTTTTCCCCCTTACTTTCTGGGGTGGACATCCAA
 att
 attB 3' LTR
 3' LTR MoMLV

NheI
 GGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTC
 CGGTTTCGATCGAATTCATTGCGGTAAAACGTTCCGTACCTTTTATGTATTGACTCTTATCTCTTCAAGTCTAGTTCCAG
 3' LTR
 3' LTR MoMLV

PvuII EcoRV
 AGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTGCCCCGGCTCAGGGCCAAGAA
 TCCTTGCTACCTTGTCGACTTATACCCGGTTTGTCTATAGACACCATTCGTCAAGGACGGGGCCGAGTCCCGGTTCTT
 3' LTR
 3' LTR MoMLV

PvuII EcoRV
 CAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTGCCCCGGCTCAGGGCCAAGAACAGAT
 GTCTACCTTGTCGACTTATACCCGGTTTGTCTATAGACACCATTCGTCAAGGACGGGGCCGAGTCCCGGTTCTTGTCTA
 3' LTR
 3' LTR MoMLV

FIG. 14 (cont)

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GD2407 pLNBLV-YFP Map.MPD (1 > 7010) Site and Sequence

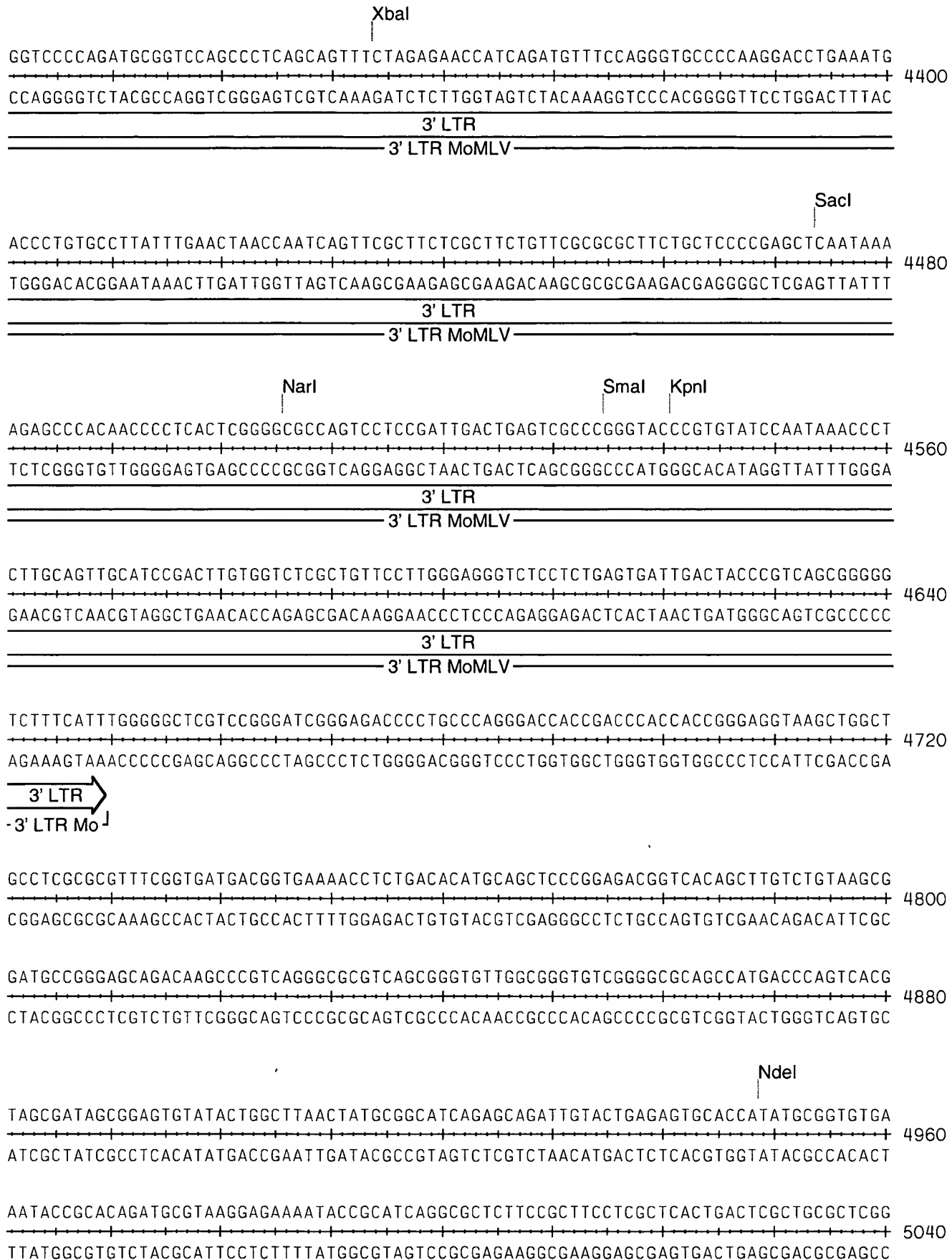


FIG. 14 (cont)

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GD2407 pNLBV-YFP Map.MPD (1 > 7010) Site and Sequence

TCGTTCCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGA
5120
AGCAAGCCGACGCCGCTCGCCATAGTCGAGTGAGTTTCCGCCATTATGCCAATAGGTGTCTTAGTCCCCTATTGCGTCTT

AAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCG
5200
TTCTTGTAACACTCGTTTTCCGGTCGTTTTCCGGTCCTTGGCATTTCCTGGCGCAACGACCGCAAAAAGGTATCCGAGGC



CCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGT
5280
GGGGGACTGCTCGTAGTGTTTTAGCTGCGAGTTCAGTCTCCACCGCTTTGGGCTGTCTGATATTTCTATGGTCCGCA

TTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCG
5360
AAGGGGACCTTCGAGGGAGCACGCGAGAGGACAAGGCTGGGACGGCGAATGGCCTATGGACAGGCGGAAAGAGGGAAGC

GGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGT
5440
CCTTCGCACCGCGAAAGAGTATCGAGTGCGACATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTCGACCCGACACA

GCACGAACCCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACT
5520
CGTGCTTGGGGGCAAGTCGGGCTGGCGACGCGGAATAGGCCATTGATAGCAGAACTCAGGTTGGGCCATTCTGTGCTGA

TATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGG
5600
ATAGCGGTGACCGTCGTCGGTGACCATTTGTCTAATCGTCTCGCTCCATACATCCGCCACGATGTCTCAAGAACTTCACC

TGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGT
5680
ACCGGATTGATGCCGATGTGATCTTCTGTCTATAAACCATAGACGCGAGACGACTTCGGTCAATGGAAGCCTTTTCTCA

TGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAA
5760
ACCATCGAGAACTAGGCCGTTTGTGTTGGTGGCGACCATCGCCACCAAAAAACAAACGTTTCGTCTAATGCGCGTCTT

AAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACACGTTAAGGGATT
5840
TTTTTCTAGAGTTCTTCTAGGAACTAGAAAAGATGCCCCAGACTGCGAGTCACCTTGCTTTTGAGTGCAATTCCCTAA

BspHI

DraI

DraI

TTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAATAATGAAGTTTTAAATCAATCTAAAGTAT
5920
AACCAGTACTCTAATAGTTTTTCTAGAAAGTGGATCTAGGAAAATTAATTTTTACTTCAAATTTAGTTAGATTTTCATA

ATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCAT
6000
TATACTCATTTGAACCAGACTGTCAATGGTTACGAATTAGTCACTCCGTGGATAGAGTCGCTAGACAGATAAAGCAAGTA

• Trp His Lys Ile Leu Ser Ala Gly Ile Glu Ala Ile Gln Arg Asn Arg Glu Asp
b-Lactamase

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GD2407 pNLBV-YFP Map.MPD (1 > 7010) Site and Sequence

CCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATA
 6080
 GGTATCAACGGACTGAGGGGCAGCACATCTATTGATGCTATGCCCTCCCGAATGGTAGACCGGGTCACGACGTTACTAT
 Met Thr Ala Gln Ser Gly Thr Thr Tyr Ile Val Val Ile Arg Ser Pro Lys Gly Asp Pro Gly Leu Ala Ala Ile Ile
 b-Lactamse

CCGCGAGACCCACGCTCACC GGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCC
 6160
 GGGCTCTGGGTGCGAGTGCGCGAGGTCTAAATAGTCGTTATTTGGTCGGTCGGCCTTCCCGGCTCGCGTCTTACCAGG
 Gly Arg Ser Gly Arg Glu Gly Ala Gly Ser Lys Asp Ala Ile Phe Trp Gly Ala Pro Leu Ala Ser Arg Leu Leu Pro Gly
 b-Lactamse

TGCAACTTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGC
 6240
 ACGTTGAAATAGGCGGAGGTAGGTCAGATAATTAACAACGGCCCTTCGATCTCATTTCATCAAGCGGTCAATTATCAAACG
 Ala Val Lys Asp Ala Glu Met Trp Asp Ile Leu Gln Gln Arg Ser Ala Leu Thr Leu Leu Glu Gly Thr Leu Leu Lys Arg
 b-Lactamse

GCAACGTTGTTGCCATTGCTGCAGGCATCGTGGTGTACGCTCGTCGTTTGGTATGGCTTCATTTCAGCTCCGGTTCCCAA
 6320
 CGTTGCAACAACGGTAACGACGTCCGTAGCACCACAGTGCAGCAGCAAACCATACCGAAGTAAGTCGAGGCCAAGGGTT
 Leu Thr Thr Ala Met Ala Ala Pro Met Thr Thr Asp Arg Glu Asp Asn Pro Ile Ala Glu Asn Leu Glu Pro Glu Trp
 b-Lactamse

CGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTGAGAAG
 6400
 GCTAGTTCCGCTCAATGTACTAGGGGGTACAACACGTTTTTTTCGCCAATCGAGGAAGCCAGGAGGCTAGCAACAGTCTTC
 Arg Asp Leu Arg Thr Val His Asp Gly Met Asn His Leu Phe Ala Thr Leu Glu Lys Pro Gly Gly Ile Thr Thr Leu Leu
 b-Lactamse

TAAGTTGGCCGAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCT
 6480
 ATTCAACCGGCGTCACAATAGTGAGTACCAATACCGTCGTGACGTATTAAGAGAATGACAGTACGGTAGGCATTCTACGA
 Leu Asn Ala Ala Thr Asn Asp Ser Met Thr Ile Ala Ala Ser Cys Leu Glu Arg Val Thr Met Gly Asp Thr Leu His Lys
 b-Lactamse

TTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCA
 6560
 AAAGACACTGACCACTCATGAGTTGGTTACAGTAAGACTCTTATCACATACGCCGCTGGCTCAACGAGAACGGGCCGAGT
 Glu Thr Val Pro Ser Tyr Glu Val Leu Asp Asn Gln Ser Tyr His Ile Arg Arg Gly Leu Gln Glu Gln Gly Ala Asp
 b-Lactamse

ACACGGGATAATACCGGCCACATAGCAGAACTTTAAAAGTGCTCATTCATTGGAAAACGTTCTTCGGGGCGAAAACCTCTC
 6640
 TGTGCCCTATTATGGCGCGGTGTATCGTCTTGAAATTTTACAGAGTAGTAACCTTTTGCAAGAAGCCCCGCTTTTGAGAG
 Val Arg Ser Leu Val Ala Gly Cys Leu Leu Val Lys Phe Thr Ser Met Met Pro Phe Arg Glu Glu Pro Arg Phe Ser Glu
 b-Lactamse

Thursday, June 13, 2002 3:42 PM

GD2407 pLNBLV-YFP Map.MPD (1 > 7010) Site and Sequence

AAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTACTTTCA
 TTCCTAGAATGGCGACAACCTCTAGGTCAAGCTACATTGGGTGAGCACGTGGGTTGACTAGAAGTCGTAGAAAATGAAAGT
 Leu Ile Lys Gly Ser Asn Leu Asp Leu Glu Ile Tyr Gly Val Arg Ala Gly Leu Gln Asp Glu Ala Asp Lys Val Lys Val
 b-Lactamse

CCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATA
 GGTGCGAAAGACCCACTCGTTTTTGTCTTCCGTTTTACGGCGTTTTTCCCTTATTCCCGCTGTGCCTTTACAACCTTAT
 Leu Thr Glu Pro His Ala Phe Val Pro Leu Cys Phe Ala Ala Phe Phe Pro Ile Leu Ala Val Arg Phe His Gln Ile
 b-Lactamse

BspHI

CTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTAT
 GAGTATGAGAAGGAAAAAGTTATAATAACTTCGTAAATAGTCCCAATAACAGAGTACTCGCCTATGTATAAACTTACATA

Ser Met
 -b-Lac

BspHI

TTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCA
 AATCTTTTTATTGTTTATCCCCAAGGCGCGTGTAAGGGGCTTTTCACGGTGGACTGCAGATTCTTTGGTAATAATAGT

TGACATTAACCTATAAAAAATAGGCGTATCACGAGGCCCTTTTCGTCTTCAA
 ACTGTAATTGGATATTTTTATCCGCATAGTGCTCCGGGAAAGCAGAAGTT 7010

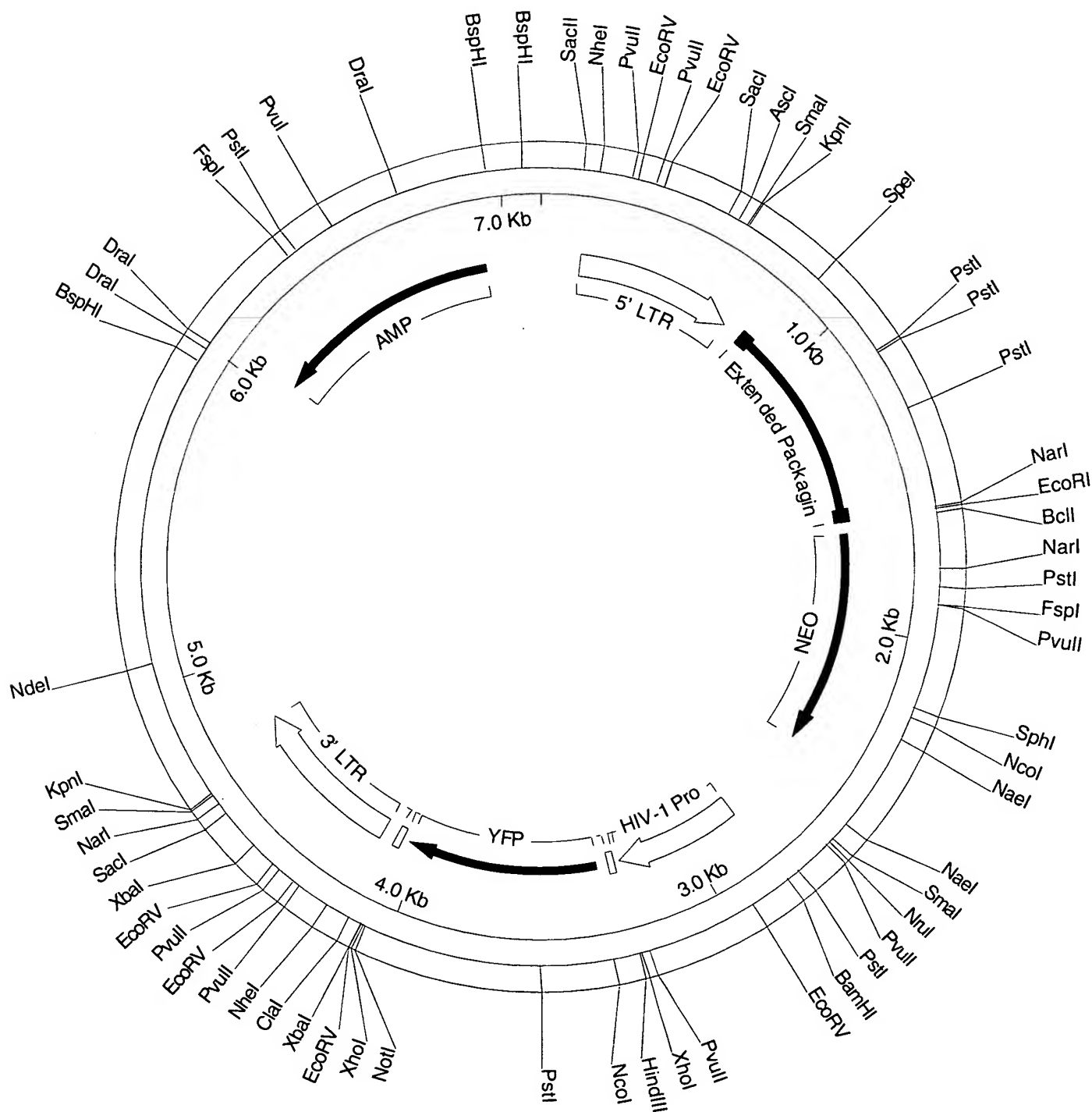


FIG. 15

FIG. 16

Page 1

Tuesday, July 02, 2002 2:11 PM
pLNHiv-YFP Map.MPD (1 > 7121) Site and Sequence
Enzymes : 36 of 538 enzymes (Filtered)
Settings : Circular, Certain Sites Only, Standard Genetic Code

GAATTAATTCATACCAGATACCGAAAACTGTCTCCAAATGTGTCCCCCTCACACTCCCAAATTCGCGGGCTTCTGCCT
CTTAATTAAGTATGGTCTAGTGGCTTTTGACAGGAGGTTTACACAGGGGGAGTGTGAGGGTTTAAGCGCCCGAAGACGGA

SacII

CTTAGACCACTCTACCCTATTCCCACACTCACCGGAGCCAAAGCCGCGGCCCTTCCGTTTCTTTGCTTTTGAAAGACCC
GAATCTGGTGAGATGGGATAAGGGGTGTGAGTGGCCTCGGTTTCGGCGCCGGAAGGCAAAGAAACGAAAACTTTCTGGG

5' LTR

NheI

CACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTC
GTGGGCATCCACCGTTCGATCGAATTCATTGCGGTGAAACGTTCCGTACCTTTTTATGTATTGACTCTTATCTTTTCAAG

5' LTR

PvuII

EcoRV

AGATCAAGGTCAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGCGGTTCTTGCCCCGGCTCAGGGC
TCTAGTTCCAGTCCTTGTTTCTTTGTGCACTTATGGTTTGTCTATAGACACCATTCGCCAAGGACGGGGCCGAGTCCCG

5' LTR

PvuII

EcoRV

CAAGAACAGATGAGACAGCTGAGTGATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTTGCCCCGGCTCGGGGCCAAG
GTTCTTGCTACTCTGTGCACTCACTACCCGGTTTGTCTATAGACACCATTCGTCAAGGACGGGGCCGAGCCCCGGTTC

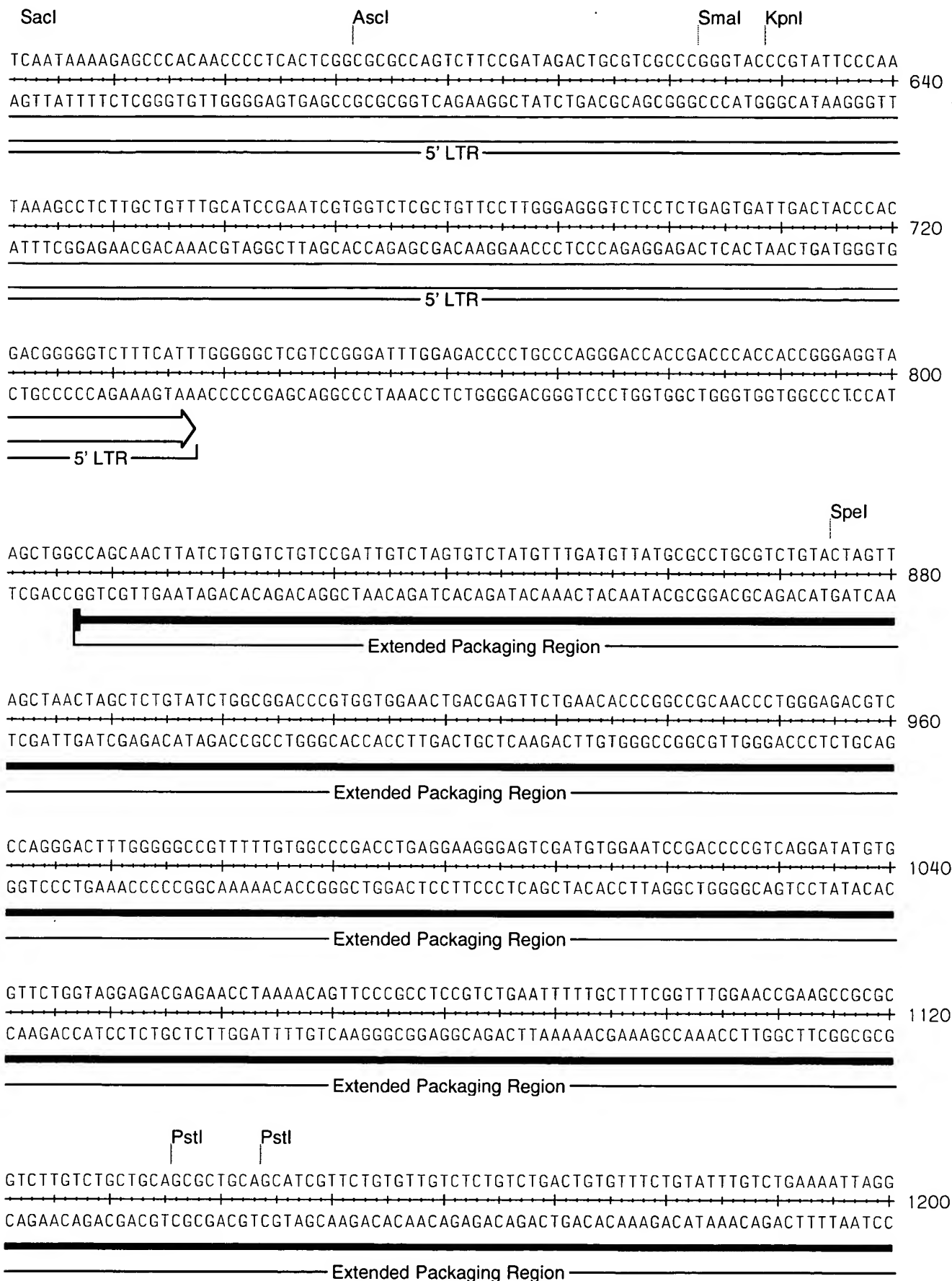
5' LTR

AACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATCATCAGATGTTTCCAGGGTGCCCCAAGGACC
TTGTCTACCAGGGGTCTACGCCAGGTGCGGAGTCGTCAAAGATCACTTAGTAGTCTACAAAGGTCCACGGGGTTCTTGG

5' LTR

TGAAAATGACCCTGTACCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCCGCTCTCCGAGC
ACTTTTACTGGGACATGGAATAAACTTGATTGGTTAGTCAAGCGAAGAGCGAAGACAAGCGCGGAAGCGGAGAGGCTCG

5' LTR



Tuesday, July 02, 2002 2:11 PM
pLNHiv-YFP Map.MPD (1 > 7121) Site and Sequence

GCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCCTGGAAGATGTCGAGCGGATCGCTCACAACCAGTCGGTA
CGGTCTGACAATGGTGAGGAATTCAAACCTGGAATCCAGTGACCTTTCTACAGCTCGCCTAGCGAGTGTGGTCAGCCAT

1280

Extended Packaging Region

PstI

GATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTGGATGGCCGCGAGACGGCAC
CTACAGTTCTTCTCTGCAACCAATGGAAGACGAGACGTCTTACCGGTTGAAATTGCAGCCTACCGGCGCTCTGCCGTG

1360

Extended Packaging Region

CTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTCTTTTACCTGGCCCCGCATGGACACCCAGACCAGGTCCCTT
GAAATTGGCTCTGGAGTAGTGGGTCCAATTCTAGTTCCAGAAAAGTGACCGGGCGTACCTGTGGGTCTGGTCCAGGGGA

1440

Extended Packaging Region

ACATCGTGACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAGCCTCCGCTCCT
TGTAGCACTGGACCTTCGGAACCGAAAACCTGGGGGAGGGACCCAGTTTCGGGAAACATGTGGGATTTCGGAGCGGAGGA

1520

Extended Packaging Region

CTTCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCAC
GAAGGAGGTAGGCGGGGCAGAGAGGGGGAACCTTGGAGGAGCAAGCTGGGGCGGAGCTAGGAGGGAAATAGGTCGGGAGTG

1600

Extended Packaging Region

NarI EcoRI BclI

TCCTTCTCTAGGCGCCGAATTCCGATCTGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTG
AGGAAGAGATCCGCGGCCTTAAGGCTAGACTAGTTCTCTGTCTACTCCTAGCAAAGCGTACTAATTGTTCTACCTAAC

1680

Extended Packaging

Met Ile Glu Gln Asp Gly Leu
NEO

CACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCCGGCTATGACTGGGCACAACAGACAATCCGGCTGCTCTGATGC
GTGCGTCCAAGAGCCGCGGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACG

1760

His Ala Gly Ser Pro Ala Ala Trp Val Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser Asp Ala
NEO

NarI

CGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCGGTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGC
GCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACG

1840

Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu
NEO

Tuesday, July 02, 2002 2:11 PM
pLNHiv-YFP Map.MPD (1 > 7121) Site and Sequence

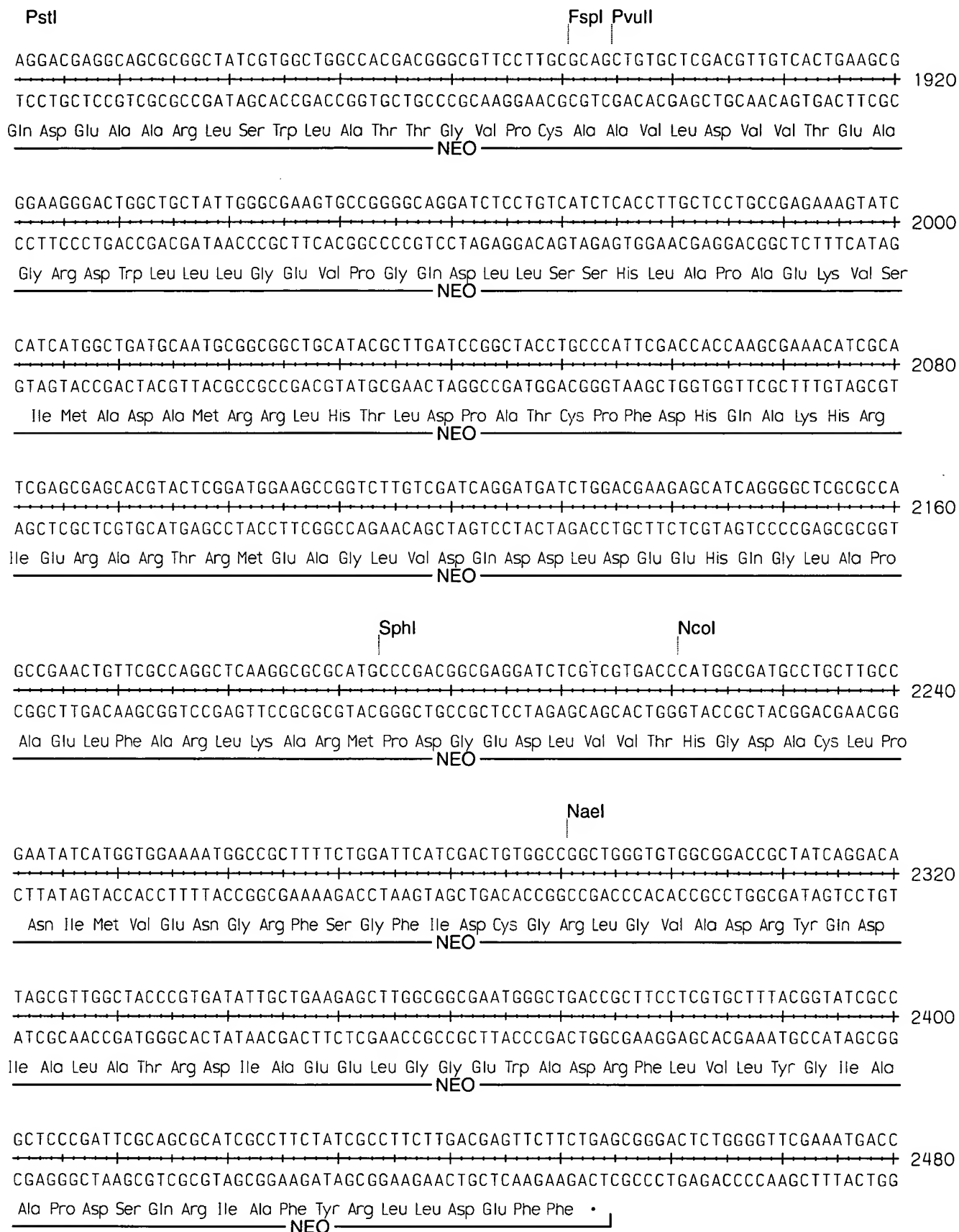


FIG. 16 (cont)

Tuesday, July 02, 2002 2:11 PM
pLNHiv-YFP Map.MPD (1 > 7121) Site and Sequence

GACCAAGCGACGCCAACCTGCCATCAGAGATTTGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCGT 2560
CTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCA

NaeI

SmaI

TTTCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCGGGCTCGATCCCC 2640
AAAGGCCCTGCGGCCGACCTACTAGGAGGTGCGGCCCTAGAGTACGACCTCAAGAAGCGGTGGGGCCCCGAGCTAGGGG

NruI

PvuII

TCGCGAGTTGGTTCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGCAAATCCGTCGGCATCCAG 2720
AGCGCTCAACCAAGTCGACGACGGACTCCGACCTGCTGGAGCGCTCAAGATGGCCGTACGTTTAGGCAGCCGTAGGTC

PstI

GAAACCAGCAGCGGCTATCCGCGCATCCATGCCCCGAAGTGCAGGAGTGGGAGGCACGATGGCCGCTTTGGTCGAGGC 2800
CTTTGGTCGTCGCCGATAGGCGCGTAGGTACGGGGGCTTGACGTCCTCACCCCTCCGTGCTACCGGCGAAACCAGCTCCG

BamHI

GGATCCTGGAAGGGCTAATTTGGTCCCAAAGAAGACAAGAGATCCTTGATCTGTGGATCTACCACACACAAGGCTACTTC 2880
CCTAGGACCTTCCCGATTAAACCAGGGTTTCTTCTGTTCTCTAGGAAC TAGACACCTAGATGGTGTGTGTTCGATGAAG

HIV-1 Promoter

EcoRV

CCTGATTGGCAGAATTACACACCAGGGCCAGGGATCAGATATCCACTGACCTTTGGATGGTGCTTCAAGCTAGTACCACT 2960
GGACTAACCCTCTTAATGTGTGGTCCCGGTCCCTAGTCTATAGGTGACTGGAAACCTACCACGAAGTTCGATCATGGTCA

HIV-1 Promoter

TGAGCCAGAGAAGGTAGAAGAGGCCAATGAAGGAGAGACAACAGCTTGTTACACCCTATGAGCCTGCATGGGATGGAGG 3040
ACTCGGTCTCTTCCATCTTCTCCGGTTACTTCTCTCTTGTGTGCAACAATGTGGGATACTCGGACGTACCCTACCTCC

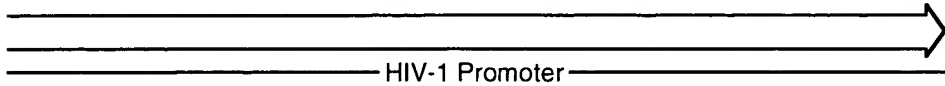
HIV-1 Promoter

ACGCGGAGAAAGAAGTGTAGTGTGGAGGTTTGACAGCAAAGTAGCATTTTCATCACATGGCCCGAGAGCTGCATCCGGAG 3120
TGCGCCTCTTTCTTCAATCACACCTCCAAAGTGTGCTTTGATCGTAAAGTAGTGTACCGGGCTCTCGACGTAGGCCTC

HIV-1 Promoter

TACTACAAAGACTGCTGACATCGAGCTTTCTACAAGGGACTTTCCGCTGGGGACTTTCCAGGGAGGCGTGGCCTGGGCGG 3200
ATGATGTTTCTGACGACTGTAGCTCGAAAGATGTTCCCTGAAAGGCGACCCCTGAAAGGTCCCTCCGCACCGGACCCGCC

HIV-1 Promoter



ACAAGTTTGTACAAAAAAGCAGGCTTCGAAGGAGATAGAACCAATTCTCTAAGGAAATACTTAACCATGGTGAGCAAGGG
TGTTCAAACATGTTTTTTCGTCCGAAGCTTCCTCTATCTTGGTTAAGAGATTCTTTATGAATTGGTACCACTCGTTCCC



CGAGGAGCTGTTACACGGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCG 3440
GCTCCTCGACAAGTGGCCCCACCACGGGTAGGACCAGCTCGACCTGCCGCTGCATTTGCCGGTGTTCAAGTCGCACAGGC
Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
YEP

GCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGG
CGCTCCCGCTCCCGCTACGGTGGATGCCGTTGCACTGGGACTTCAAGTAGACGTGGTGGCCGTTTCGACGGGCACGGGACC
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr **YEP** Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp

CAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCG 3680
GTTCAAGGCGGTACGGGCTTCCGATGCAGGTCTCGCGTGGTAGAAGAAGTTCTGCTGCCGTTGATGTTCTGGGCGCGGC
Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala

AGGTGAAGTTCGAGGGCGACACCTTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTG
TCCACTTCAAGCTCCCGCTGTGGGACCACTTGGCGTAGCTCGACTTCCCGTAGCTGAAGTTCCCTCCTGCCGTTGTAGGAC
Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu

GGGCACAAGCTGGAGTACAAC TACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAA 3840
 CCCGTGTTGACCTCATGTTGATGTTGTCGGTGTTCAGATATAGTACCGGCTGTTCTGCTTCTTGCCGTAGTTCCACTT
 Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
 YEP

Tuesday, July 02, 2002 2:11 PM
pLNHiv-YFP Map.MPD (1 > 7121) Site and Sequence

CTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACG
3920
GAAGTTCTAGGCGGTGTTGTAGCTCCTGCCGTGCACGTCGAGCGGCTGGTGATGGTCGTCTTGTGGGGGTAGCCGCTGC
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
YFP

GCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTACCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCAC
4000
CGGGGCACGACGACGGGCTGTTGGTGATGGACTCGATGGTCAGGCGGGACTCGTTTCTGGGGTTGCTCTTCGCGCTAGTG
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
YFP

ATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAAGCGGCCGCACTCG
4080
TACCAGGACGACCTCAAGCACTGGCGGCGGCCCTAGTGAGAGCCGTACCTGCTCGACATGTTTCAATTCGCCGCGTGAGC
Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
YFP

EcoRV
XbaI

Clal

AGATATCTAGACCCAGCTTTCTTGTACAAAGTGGTGATAACATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAA
4160
TCTATAGATCTGGGTCGAAAGAACATGTTTACCACACTATTGTAGCTATTTTATTTTCTAAATAAATCAGAGGTCTTTT
att B2

NheI

GGGGGAATGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGAAGGCATGGAAAAATACAT
4240
CCCCCTTACTTTCTGGGGTGGACATCCAAACGTTTCGATCGAATTCATTGCGGTAAACGTTCCGTACCTTTTATGTA
3' LTR

PvuII

EcoRV

AACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTA
4320
TTGACTCTTATCTCTCAAGTCTAGTTCAGTCCTTGTCTACCTTGTCGACTTATACCCGGTTTGTCTATAGACACCAT
3' LTR

PvuII

EcoRV

AGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAG
4400
TCGTCAAGGACGGGGCCGAGTCCCGTTCTTGTCTACCTTGTCGACTTATACCCGGTTTGTCTATAGACACCATTCGTC
3' LTR

FIG. 16 (cont)

Tuesday, July 02, 2002 2:11 PM
pLNHiv-YFP Map.MPD (1 > 7121) Site and Sequence

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XbaI

TTCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGA 4480
AAGGACGGGGCCGAGTCCCGGTTCTTGTCTACCAGGGGTCTACGCCAGGTCGGGAGTCGTCAAAGATCTCTTGGTAGTCT

3' LTR

TGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGT 4560
ACAAAGGTCCACGGGGTTCCTGGACTTTACTGGGACACGGAATAAACTTGATTGGTTAGTCAAGCGAAGAGCGAAGACA

3' LTR

SacI NarI

TCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGT 4640
AGCGCGCAAGACGAGGGGCTCGAGTTATTTTCTCGGGTGTGGGGAGTGAGCCCCGCGGTCAGGAGGCTAACTGACTCA

3' LTR

SmaI KpnI

CGCCCGGGTACCCGTGTATCCAATAAACCCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTTCTTGGGAGGGTCTC 4720
GCGGGCCCATGGGCACATAGGTTATTTGGGAGAACGTCAACGTAGGCTGAACACCAGAGCGACAAGGAACCCCTCCCAGAG

3' LTR

CTCTGAGTGATTGACTACCCGTACGCGGGGGTCTTTCATTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCAGGGAC 4800
GAGACTCACTAACTGATGGGCAGTCGCCCCAGAAAGTAAACCCCGAGCAGGCCCTAGCCCTCTGGGGACGGGTCCCTG

3' LTR

CACCGACCCACCACGGGAGGTAAGCTGGCTGCCTCGCGGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCT 4880
GTGGCTGGGTGGTGGCCCTCCATTGACCGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGGAGACTGTGTACGTCTGA

CCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCG 4960
GGGCCTCTGCCAGTGTGAACAGACATTGCCTACGGCCCTCGTCTGTTTCGGGCAGTCCCGCGCAGTCGCCACAACCGC

GGTGTCGGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGATACTGGCTTAACTATGCGGCATCAGAGCAGA 5040
CCACAGCCCCGCGTCGGTACTGGGTCAGTGCATCGCTATCGCCTCACATATGACCGAATTGATACGCCGTAGTCTCGTCT

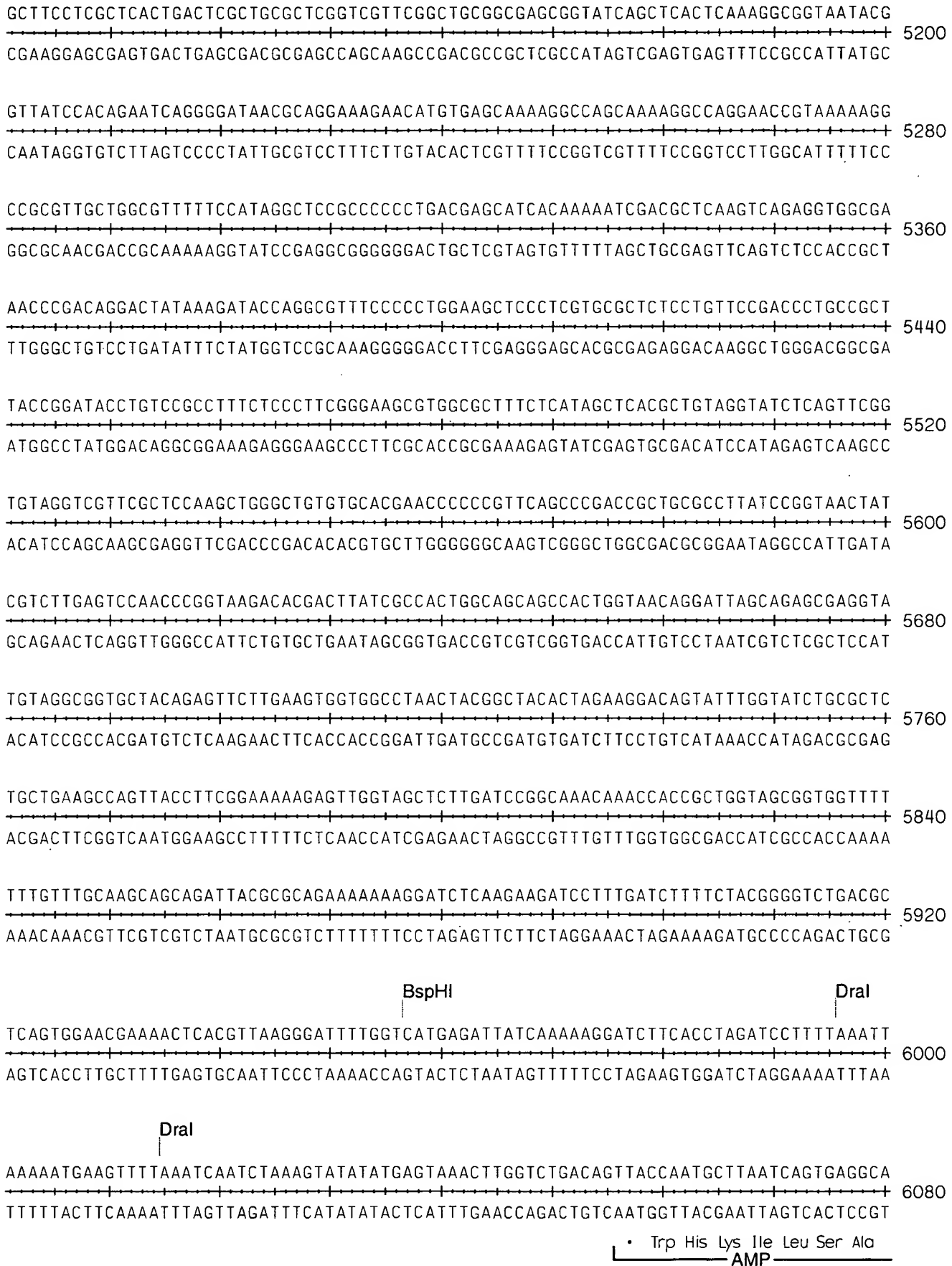
NdeI

TTGTACTGAGAGTGACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAAATACCGCATCAGGCGCTCTTCC 5120
AACATGACTCTCACGTGGTATACGCCACACTTTATGGCGTGTCTACGCATTCTCTTTTATGGCGTAGTCCGCGAGAAGG

FIG. 16 (cont)

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Tuesday, July 02, 2002 2:11 PM
pLNHiv-YFP Map.MPD (1 > 7121) Site and Sequence



Tuesday, July 02, 2002 2:11 PM
pLNHiv-YFP Map.MPD (1 > 7121) Site and Sequence

CCTATCTCAGCGATCTGTCTATTTGTTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGG
6160
GGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTATCAACGGACTGAGGGGCAGCACATCTATTGATGCTATGCCCTCCC
Gly Ile Glu Ala Ile Gln Arg Asn Arg Glu Asp Met Thr Ala Gln Ser Gly Thr Thr Tyr Ile Val Val Ile Arg Ser Pro
AMP

CTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTACCGGCTCCAGATTTATCAGCAATAAACCAGC
6240
GAATGGTAGACCGGGGTCACGACGTTACTATGGCGCTCTGGGTGCGAGTGCCGAGGTCTAAATAGTCGTTATTTGGTGC
Lys Gly Asp Pro Gly Leu Ala Ala Ile Ile Gly Arg Ser Gly Arg Glu Gly Ala Gly Ser Lys Asp Ala Ile Phe Trp Gly
AMP

CAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCT
6320
GTCGGCCTTCCCGGCTCGCGTCTTACCAGGACGTTGAAATAGCGGAGGTAGGTACAGATAATTAACAACGGCCCTTCGA
Ala Pro Leu Ala Ser Arg Leu Leu Pro Gly Ala Val Lys Asp Ala Glu Met Trp Asp Ile Leu Gln Gln Arg Ser Ala
AMP

FspI PstI
AGAGTAAGTAGTTCCGCGTAAATAGTTTGCACAACGTTGTTGCCATTGCTGCAGGCATCGTGGTGTACGCTCGTCGTT
6400
TCTCATTCAATCAAGCGGTCAATTATCAAACGCGTTGCAACAACGGTAACGACGTCCGTAGCACCACAGTGCAGCAGCAA
Leu Thr Leu Leu Glu Gly Thr Leu Leu Lys Arg Leu Thr Thr Ala Met Ala Ala Pro Met Thr Thr Asp Arg Glu Asp Asn
AMP

TGGTATGGCTTCATTACGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTA
6480
ACCATACCGAAGTAAGTCGAGGCCAAGGGTTGCTAGTTCCGCTCAATGTACTAGGGGTACAACACGTTTTTTCGCCAAT
Pro Ile Ala Glu Asn Leu Glu Pro Glu Trp Arg Asp Leu Arg Thr Val His Asp Gly Met Asn His Leu Phe Ala Thr Leu
AMP

PvuI
GCTCCTTCGGTCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCGAGTGTATCACTCATGGTTATGGCAGCACTGCATAAT
6560
CGAGGAAGCCAGGAGGCTAGCAACAGTCTTCAATTCAACCGGCGTCACAATAGTGAGTACCAATACCGTCGTGACGTATTA
Glu Lys Pro Gly Gly Ile Thr Thr Leu Leu Leu Asn Ala Ala Thr Asn Asp Ser Met Thr Ile Ala Ala Ser Cys Leu
AMP

TCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTAT
6640
AGAGAATGACAGTACGGTAGGCATTCTACGAAAAGACACTGACCACTCATGAGTTGGTTTCAGTAAGACTCTTATCACATA
Glu Arg Val Thr Met Gly Asp Thr Leu His Lys Glu Thr Val Pro Ser Tyr Glu Val Leu Asp Asn Gln Ser Tyr His Ile
AMP

DraI
GCGGCGACCGAGTTGCTCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAGTGCTCATCA
6720
CGCCGCTGGCTCAACGAGAACGGGCGCAGTTGTGCCCTATTATGGCGCGGTGTATCGTCTTGAAATTTTCACGAGTAGT
Arg Arg Gly Leu Gln Glu Gln Gly Ala Asp Val Arg Ser Leu Val Ala Gly Cys Leu Leu Val Lys Phe Thr Ser Met Met
AMP

FIG. 16 (cont)

Tuesday, July 02, 2002 2:11 PM
pLNHiv-YFP Map.MPD (1 > 7121) Site and Sequence

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TTGGAACGTTCTTCGGGGCGAAACCTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCA
AACCTTTTGCAAGAAGCCCGCTTTTGGAGAGTTCTAGAAATGGCGACAACCTTAGGTCAAGCTACATTGGGTGAGCACGT
Pro Phe Arg Glu Glu Pro Arg Phe Ser Glu Leu Ile Lys Gly Ser Asn Leu Asp Leu Glu Ile Tyr Gly Val Arg Ala
AMP

CCCAACTGATCTTCAGCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAACAGGAAGGCAAAATGCCGCAAAAAA
GGGTTGACTAGAGTCGTAGAAAATGAAAGTGGTCGAAAGACCCACTCGTTTTTGTCTTCCGTTTTACGGCGTTTTTT
Gly Leu Gln Asp Glu Ala Asp Lys Val Lys Val Leu Thr Glu Pro His Ala Phe Val Pro Leu Cys Phe Ala Ala Phe Phe
AMP

GGGAATAAGGGCGACACGAAATGTTGAATACTCATCTCTTCTTTTCAATATTATTGAAGCATTATCAGGGTTATT
CCCTTATCCCGCTGTGCCCTTACAACCTATGAGTATGAGAAGGAAAAAGTTATAATACTTCGTAAATAGTCCCAATAA
Pro Ile Leu Ala Val Arg Phe His Gln Ile Ser Met
AMP

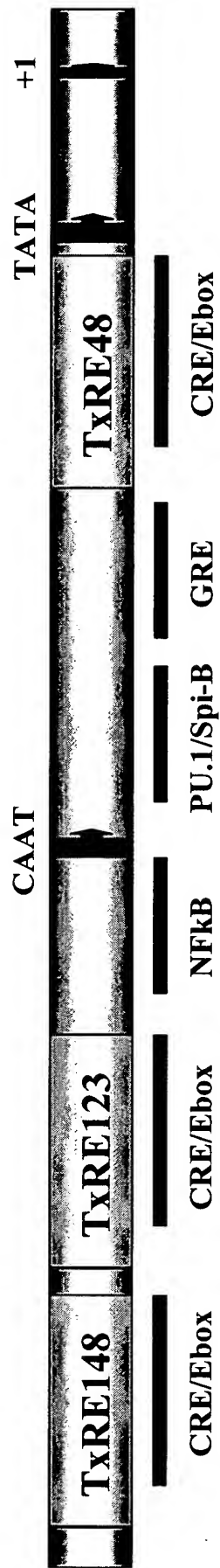
BspHI

GTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTG
CAGAGTACTCGCCTATGTATAAACTTACATAAATCTTTTTATTTGTTTATCCCCAAGGCGCGTGTAAGGGGCTTTTCAC

BspHI

CCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAAATAGGCGTATCACGAGGCCCTTTTCGTCTTCA
GGTGGACTGCAGATTCTTTGGTAATAATAGTACTGTAATTGGATATTTTATCCGCATAGTGCTCCGGGAAAGCAGAAGT

A
> 7121
T



BLV promoter

FIG. 17

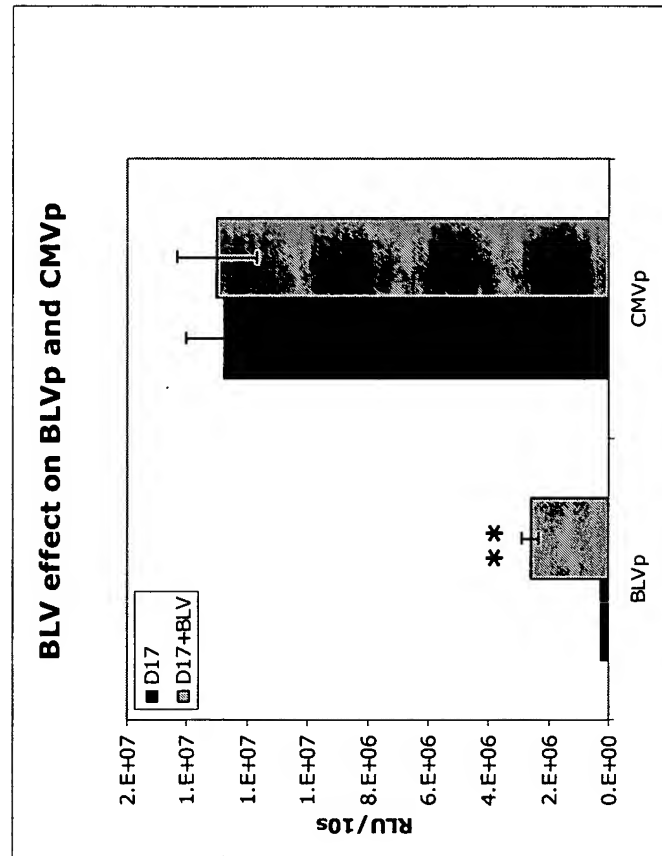


FIG. 19

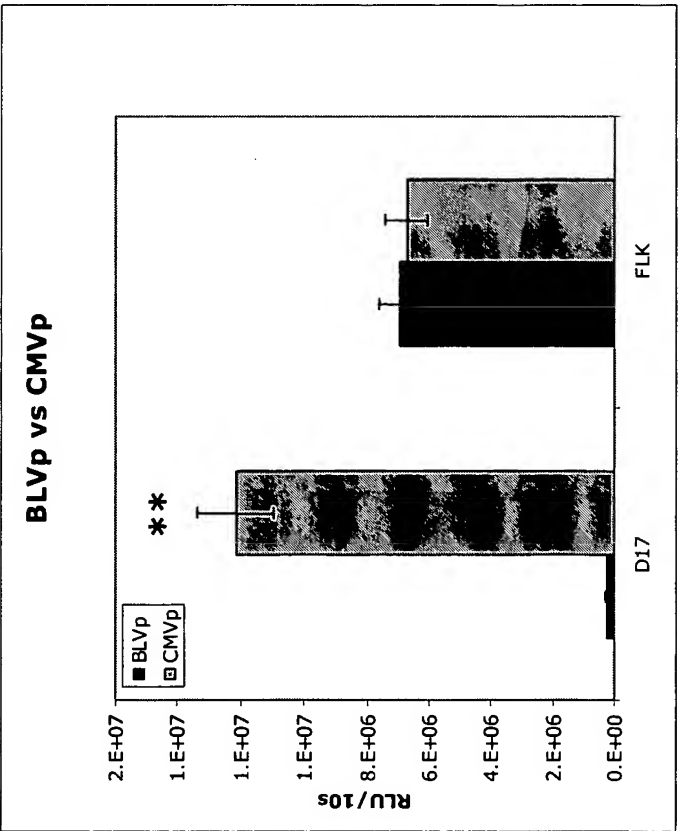


FIG. 18A

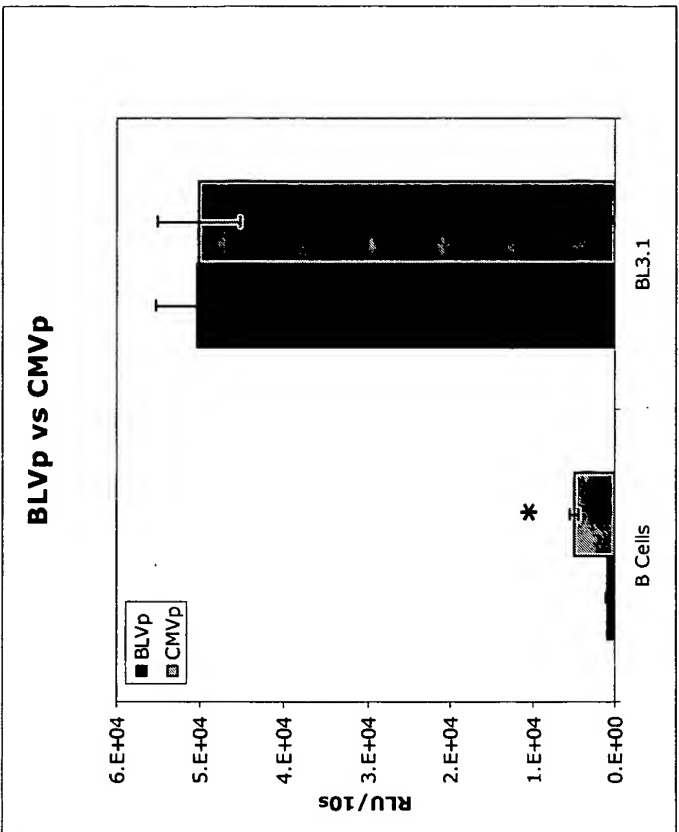


FIG. 18B

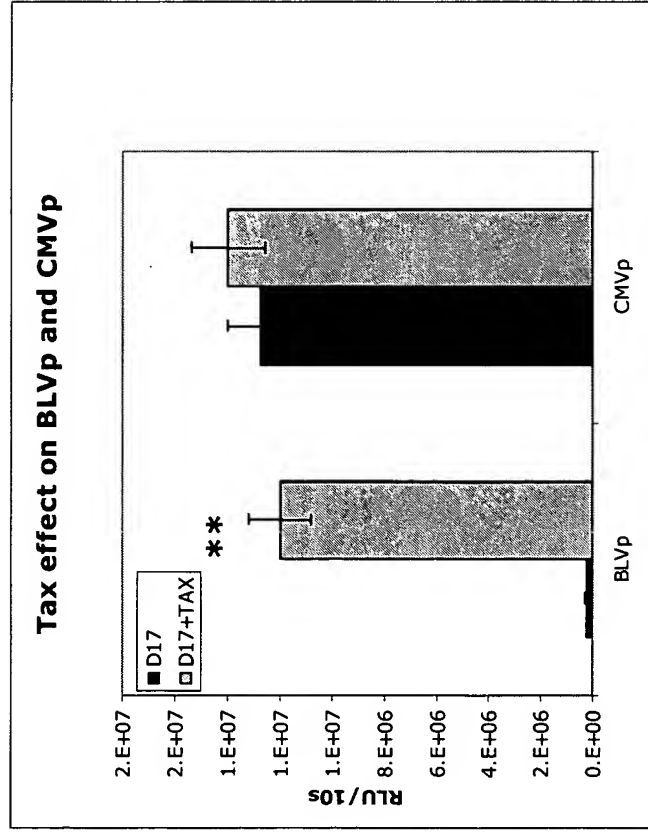


FIG. 20A

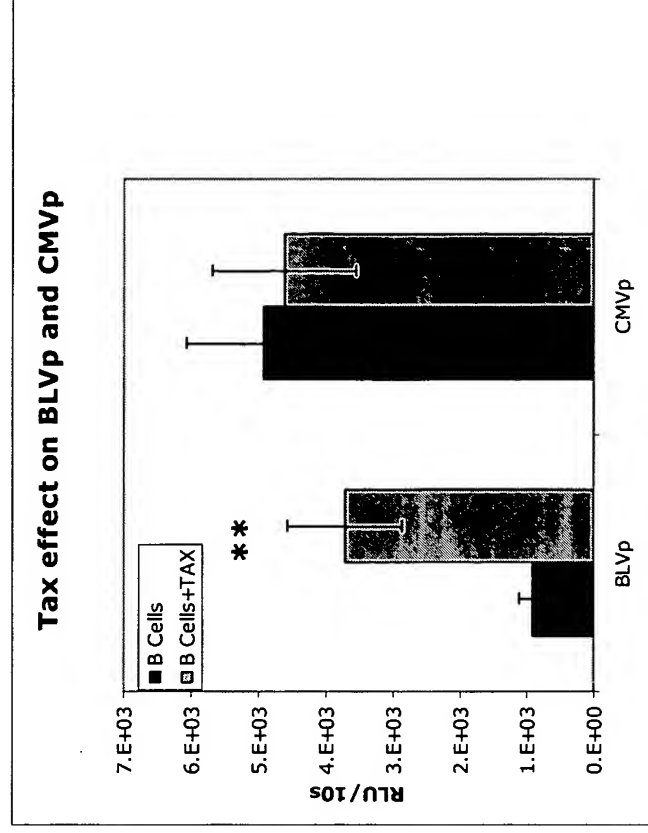


FIG. 20B